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GenCore version 5.1.6
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OM protein - protein search, using sw model

March Run on:

7, 2005, 07:19:47; Search time 10.1722 Seconds (without alignments) 151.341 Million cell updates/sec

US-10-001-938-3 Perfect score:

1 OKRAAYDQYGHAAFEQ 16 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 seg seg 88 Minimum I Maximum I Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl: \* 2: pirl: \* 3: pirl: \* 4: pir4: \* PIR 79:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	ID Description	HHECDJ heat shock protein	G90630 DnaJ protein [impo	rone wit	AF0503 DnaJ protein (impo	chape	heat	dnaJ protein	nolC	dnaJ	heat	D81242 DnaJ protein NMA02	heat	chaperone	molecular	AC3502 chaperone protein		C71729 dnaJ protein (dnaJ	E70361 chaperone DnaJ -	heat shock pr	DnaJ protein	dnaJ protein	DnaJ protein	heat shock pr	dnaJ protei	A49210 heat shock protein	D70164 heat shock protein	11 heat shock	44-	T43/39 near snock protein
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	Query Match Length I	376	376	376	379	379	394	381	392	377	377	373	375	377	377	377	367	370	376	190	377	373	379	379	385	352	364	376	200	
d	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	96.5	95.3	87.2	87.2	84.9	84.9	84.9	4.	84.9	74.4	74.4	73.3	72.1	72.1	69.8	67.4	67.4		9	66.3	66.3	2	9
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	Result No.	7	8	m	4	Ŋ	y	7	œ	თ	10	11	12	13		15		17	18	19	20	21	22	23	24	25	56	27	28	2

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F82570 H97928 D95060	G96831 B41874 H69038 S41748 G81329	T04618 B89939 E90603 F71379	T48161 B84602 D83818 D82894
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368 372 378	499 372 376 389 299	348 379 383 416	335 346 370 375
65.1 65.1 65.1	61.6 60.5 60.5 58.1	58.1 58.1 58.1	57.0 57.0 57.0
50 50	22223	200	4 4 4 4 0 0 0 0
30 31 32	3 3 4 4 3 4 4 3 4 4 4 4 4 4 4 4 4 4 4 4	38 39 44 11	4 4 4 4 4 4 2 2 4 4 4 4 4 4 4 4 4 4 4 4

# ALIGNMENTS

	S
	Escherichia
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	dnaJ
	: protein
1 1 1	shock
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li (strain K-12) C;Species: Escherichia coli

C;Date: 30-Jun-1988 #sequence revision 30-Jun-1988 #text\_change 09-Jul-2004 C;Accession: A92572; A26298; \$40537; G64721; A26299 R;Bardwell, J.C.A.; Tilly, K.; Craig, E.; King, J.; Zylicz, M.; Georgopoulos, J. Biol. Chem. 261, 1782-1785, 1986 A;Tille: The nucleotide sequence of the Escherichia coli K12 dnaJ gene. A;Reference number: A92572; MUID:86111850; PMID:3003085

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A; Accession: A92572

A; Molecule type: DNA A; Residues: 1-376 < BAR>

, Cross-references: UNIPROT:P08622, GB:M12565, NID:g145767, PIDN:AAA23693.1, PID:g145769 , Experimental source: strain K12

Rjohki, M.; Tamura, F.; Nishimura, S.; Uchida, H. 7. Biol. Chem. 251, 1778-1781, 1986 A;Title: Nucleotide sequence of the Escherichia coli dnaJ gene and purification of the A;Reference number: A26298; MUID:86111849; PMID:3003084

A; Residues: 1-376 <OHK> , Molecule type: DNA ;Accession: A26298

A;Cross-references: GB:D10483; GB:J01597; GB:J01683; GB:J01706; GB:K01298; GB:K01990; GB
R;Yura, T.; Mori, H.; Magai, H.;

A; Reference number: \$40531 A; Accession: \$40537

A; Molecule type: DNA
A; Residues: 1-376 «VUR»
A; Residues: 1-376 «VUR»
A; Residues: 1-376 «VUR»
A; Roses-references: EMBL: D10483; NID: 9216434; PIDN: BAA01292.1; PID: 9216441
A; Roses-references: EMBL: D10483; NID: 9164, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co.Science 277, 1453-1462, 1997
A; Roses 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID: 97426617; PMID: 9278503

A; Molecule type: DNA

A; Status: nucleic acid sequence not shown; translation not shown Accession: G64721

1-376 <BLAT> A;Residues:

A; ross\_references: GB:AE000112; GB:U00096; NID:g1786192; PIDN:AAC73126.1; PID:g1786197; A; Experimental source: strain K-12, substrain MG1655 C; Comment: This protein is induced by heat shock under the control of the htpR gene prod

C; Superfamily: hear shock protein dnaJ; dnaJ amino-terminal homology
C; Keywords: DNA replication; heat shock; molecular chaperone; stress-induced protein
F;5-70/Domain: dhaJ amino-terminal homology <DNJ>
F;77-106/Region: G/F motif
F;144-151/Region: CXXXXXXX repeat
F;161-168/Region: CXXXXXXX repeat A; Map position: 0 min

Score 86; DB 1; I Pred. No. 2.7e-07; 0; Mismatches

100.0%;

Query Match Best Local Similarity

F;183-190/Region: CXXCXGXG repeat F;197-204/Region: CXXCXGX repeat

1 OKRAAYDQYGHAAFEQ 16

à 셤

16, Conservative

OKRAAYDOYGHAAFEO 76

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C; Accession: AF0503
R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Tille: Complete genome sequence of a multiple drug resistant Salmonella enterica serove A; Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R.Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B., deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Ill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, F. Nature 413, 523-527, 2001.

A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360
enterica serovar Typhi (strain CT18)
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A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
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A;Residues: 1-379 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD01166.1; PID:g16501296; GSPDB:GN00176
C;Genetics:
                                  C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 20-Aug-1999
C;Accession: C64112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB0058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: STY0013
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chaperone protein DnaJ [imported] - Yersinia pestis (strain CO92)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 86; DB 2; I 100.0%; Pred. No. 2.8e-07;
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Pred. No. 2.8e-07;
   - Salmonella enterica subsp.
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Best Local Similarity 100.0%; Pred. No. 2.8
Matches 16; Conservative 0; Mismatches
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Matches 16; Conservative
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A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Secherichia coli
C;Species: Becharichia coli
C;Date: 18-Dul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: G90630
S;Hayashi, T:, Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Accession: G90630
A;Status: preliminary
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-376 <STO>
A;Cross-references: UNIPROT:Q8XA65; UNIPROT:Q8FLC5; GB:AE005174; NID:g12512693; PIDN:AAG
A;Experimental source: strain O157:H7, substrain EDL933
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(885481
chapter with DnaK, heat shock protein [imported] - Escherichia coli (strain O157:H7, s C;Species: Escherichia coli
C;Species: Bscherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession (865481)
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhev iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoušis, K.; Apodaca, A;Title: Genome sequence of enterchemorrhagic Escherichia coli O157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA **

A;Residues: 1-37 c.HAX-*

A;Residues: 1-37 c.HAX-*

A;Cross-references: UNIPROT:Q8XA65; UNIPROT:Q8FLC5; GB:BA000007; PIDN:BAB33438.1; PID:g1

A;Experimental source: strain O157:H7, substrain RIMD 0509952
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G90630
DnaJ protein [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
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A;Gene: ECg0015
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
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OKRAAYDOYGHAAFEQ 16

8 g

OKRAAYDOYGHAAFEQ 76

1 OKRAAYDOYGHAAFEO 16 

RESULT 4

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Query Match Best Local Similarity Local 16; Conserve

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A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A!
A;Reference number: A84930; MUID:20445173; PMID:10993077
A;Accession: F84947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: JC5609
R;Sato, S.; Ishikawa, H.
J. Biochem. 122, 41-48, 1997
A;Title: Structure and expression of the dnaKJ operon of Buchnera, an intracellular symb A;Reference number: JC5608; MUID:97420684; PMID:9276669
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   A;Cross-references: UNIPROT:P26508; GB:L03521; NID:g152353; PIDN:AAA26333.1; PID:g152354 C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology F;4-69/Domain: dnaJ amino-terminal homology <DNJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: F84947
As:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         heat shock protein dnaJ - Buchnera sp.
C;Species: Buchnera sp.
C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
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                                                                                                                             Length 392;
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86.7%; Pred. No. 2.3e-05;
iive 2; Mismatches 0;
                                                                                                                             Query Match 95.3%; Score 82; DB 2; I Best Local Similarity 93.8%; Pred. No. 1.4e-06; Matches 15; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 87.2%; Score 75; DB 2; 1 Best Local Similarity 86.7%; Pred. No. 2.3e-05; Matches 13; Conservative 2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dnaJ protein [imported] - Buchnera sp. (strain APS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: GB: AP000398; GSPDB: GN00144
                                                                                                                                                                                                                                                                                           60 QKRAAYDRYGHAAFEQ 75
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F;162-169/Region: CXXCXGXG repeat
F;184-191/Region: CXXCXGXG repeat
F;198-205/Region: CXXCXGX repeat
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-377 <STO>
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A;Gene: dnaJ; BU152
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A,Gene: dnaJ
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Only Protein - Rhizobium fredii
C;Species: Rhizobium fredii
C;Species: Rhizobium fredii
C;Date: 21-Nov-1993 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Date: 21-Nov-1993 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Datesion: S15295
R;Krishnan, H.B.; Pueppke, S.G.
Mol. Microbiol. 5, 737-745, 1991
A;Title: noLC, as Rhizobium fredii gene involved in cultivar-specific nodulation of soybe
A;Reference number: S15295; MUID:91260457; PMID:1646377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:034242; GB:AE004171; GB:AE003852; NID:g9655308; PIDN:AAF9401
A;Experimental source: serogroup 01; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gispecies: Vibrio cholerae (strain N16961 serogroup O1) Cispecies: Vibrio cholerae (cipacies: Vibrio cholerae) Cipacesion: D82270 Cipacesion: D82270 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Arture 406, 477-483, 2000 A.Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833; PMID:10952301
                          A.Accession: C64112
A.Status: nucleic acid sequence not shown; translation not shown
A.Molecule type: DNA
A.Residues: 1-394 < TIGR>
A.Cross-references: GB:L42023; GB:U32803; NID:g1574162; PIDN:AAC22890.1; PID:g1574168;
A.Cross-references: GB:L42023; GB:U32803; NID:g1574162; PIDN:AAC22890.1; PID:g1574168;
A.Gene: dnaJ
A.Start codon: GTG
C.Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
C.Keywords: DNA replication; heat shock; molecular chaperone; stress-induced protein
F.17-82/Domain: dnaJ amino-terminal homology < DNJ>
F.89-121/Region: G/F motif
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C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
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A; Reference number: A64000; MUID:95350630; PMID:7542800
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Best Local Similarity 93.8%; Pred. No. 9.3e-07;
Matches 15; Conservative 1; Mismatches 0.
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Fi176-183/Region: CXXCXGXG repeat
Fi198-205/Region: CXXCXGXG repeat
Fi212-219/Region: CXXCXGXG repeat
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Best Local Similarity 100.0
Matches 16; Conservative
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A,Molecule type: DNA
A,Residues: 1-392 <MOL>
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A;Molecule type: DNA
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Length 375;

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1 OKRAAYDQYGHAAFE 15
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61 OKRAAYDRFGHAAFE 75
                                                                                                                                                                                                1 OKRAAYDOYGHAAFE 15
                                                                                                                                                                                                                                                                             60 OKRAAYDRFGHAAFE 74
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Best Local Similarity 86.7
Matches 13; Conservative
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                                                                        Best Local Similarity 86.7
Matches 13; Conservative
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Matches 13; Conserva
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A;Molecule type: DNA
A;Residues: 1-377 <KUR>
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A;Molecule type: DNA
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                                      Query Match
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B47042

heat worker protein dnaJ - Brucella ovis

C; Species: Brucella ovis

C; Species: Brucella ovis

C; Date: 21-Sep-1933 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

R; Cellier, M.F.; Teyssier, J.; Nicolas, M.; Liautard, J.P.; Marti, J.; Sri Widada, J.

A; Rcellier, M.F.; Teyssier, J. 1992

A; Reference number: A47042; MulD:93094135; PMD:1459952

A; Reference number: A47042; MulD:93094135; PMD:1459952

A; Residues: 1-375 cCEL>

A
                                                                                                                                                                                                                          Discretin NMA0209 [imported] - Neisseria meningitidis (strain MCS8 serogroup B, strain C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Accession: D81242, C82015
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.R Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Attelere Genome sequence of Neisseria meningitidis serogroup B strain MCS8.
A;Reference number: A81000; MUID:20175755; PMID:10710307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: UNIPROT:P57107; GB:AE002366; GB:AE002098; NID:g7225284; PIDN:AAF4052
A;Experimental source: serogroup B, strain MC58
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
B;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-373 <PAR>
A;Cross-references: GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CAB83522.1; PID:g737897
A;Experimental source: serogroup A, strain 22491
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A;Gene: dnaJ; NMB0059; NMA0209
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
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Pred. No. 5.1e-05;
1; Mismatches 1;
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86.7%;
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EKRSAYDQYGHAAFE 75
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Cjaccession: AD2591
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, I.; Wood, G.E.; Chen, Y.; Woo, L. R;Wood, D.W.; Setubal, J.C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellal; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Fl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-377 <KUR>
A;Residues: ISTO - KUR>
A;Cross-references: UNIPROT:P50018; GB:AE008688; PIDN:AAL41146.1; PID:g17738442; GSPDB:GN |
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume
A;Reference number: A97159; MUID:21608551; PMID:11743194
A;Accession: D97373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   molecular chaperone, DnaJ family dnaJ [imported] - Agrobacterium tumefaciens (strain CS8, C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P50018; GB:AE007869; PIDN:AAK85941.1; PID:g15154994; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                          chaperone protein dnaJ [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Species: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: D97373
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
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A;Map position: circular chromosome
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
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86.7%; Pred. No. 5.2e-05;
tive 2; Mismatches 0; Indels
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84.9%; Score 73; DB 2; I
86.7%; Pred. No. 5.2e-05;
iive 2; Mismatches 0;
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ACISON
Chaperone protein dnad [imported] - Brucella melitensis (strain 16M)
Chaperone protein dnad [imported] - Brucella melitensis (strain 16M)
Chaperone Brucella melitensis
Chacession: ACISON
Charman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 43-448, 2002
A; Riference number: AD3222; PMID:11756688
A; Reference number: AD3222; PMID:11756688
A; Actasus: Preliminary
A; Actasus: Preliminary
A; Actasus: Preliminary
A; Residues: L.377 cxUR>
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A; Residues: L.377 cxUR>
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A; Rapp position: I
C; Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
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84.9%; Score 73; DB 2; Length 377;
Best Local Similarity 86.7%; Pred. No. 5.2e-05;
Matches 13; Conservative 2; Mismatches 0; Indels
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Search completed: March 7, 2005, 07:42:13 Job time : 10.1722 secs

1 QKRAAYDQYGHAAFE 15 ||||||||::|||||| 60 QKRAAYDRFGHAAFE 74

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

March 7, 2005, 07:21:08 ; Search time 65.5894 Seconds (without alignments) 124.918 Million cell updates/sec

US-10-001-938-3 86 Title:
Perfect score: 8
Sequence:

1 QKRAAYDQYGHAAFEQ 16

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q7n8y3 photorhabdu	P08622 escherichia	Q7udul shigella fl			P48208 haemophilus		Q813d3 colwellia m		yersinia	Q6d0b8 erwinia car	P43735 haemophilus			Q6lua6 photobacter	034242 vibrio chol		vibrio		Q7mn84 vibrio vuln		Q92t07 rhizobium m	P26508 rhizobium f			Q98dd2 rhizobium 1		Q93s23 rhizobium t	Qency3 rhodopseudo	O08356 rhodopseudo	Q8rb67 thermoanaer
SUMMARIES	ID	Q7N8Y3	DNAJ ECOLI	<u>0</u> 70 <u>0</u> 01	QBFLC5	Q8XA65	DNAJ HAEDU	DNAJ SALTY	<u>0813</u> 53	Q66ES9	O8ZIM6	Q6D0B8	DNAJ HAEIN	Q83MH4	DNAJ ACTAC	QGLUAG	DNAJ_VIBCH	Q87RX2	Q8DF67	DNAJ_VIBHA	Q7MN84	Q65U54	Q92T07	NOLC_RHIFR	Q75WD2	DNAJ PASMU	Q98D <u>D</u> 2	DNAJ_RHILE	093823	DNAJ_RHOPA	DNAJ_RHOS7	Q8RB67
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032465 buchnera ap Q7vq13 candidatus 052065 pasteurella 089894 buchnera ap Q8k9y9 buchnera ap 00546 erysipeloth P63969 neisseria m P63969 brucella ov P50018 agrobacteri P94719 brucella me Q8k977 brucella me Q8fxx1 brucella su Q6rsn5 agrobacteri
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# ALIGNMENTS

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"Systematic sequencing of the Escherichia coli genome: analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-91187894; PubMed-1826368;
Liberek K., Marszalek J., Ang D., Georgopoulos C., Zylicz M.;
"Escherichia coli DnaJ and GrpE heat shock proteins jointly stimulate
ATPase activity of DnaK.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIDSALZ / MG1652.
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Magregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.,
                                                                                          Gaps
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MEDLINE-96291434; PubMed=8764403; DOI=10.1006/jmbi.1996.0395;
MEDLINE-96291434; PubMed=8764403; DOI=10.1006/jmbi.1996.0395;
Pellechia M., Szyperski T., Wall D., Georgopoulos C., Wuethrich K.;
"NMR structure of the J-domain and the Gly/Phe-rich region of the Bscherichia coli DnaJ chaperone.";
J. Mol. Biol. 260:236-250(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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Bardwell J.C.A., Tilly K., Craig E., King J., Zylicz M.,
Georgopoulos C.;
"The nucleotide sequence of the Escherichia coli K12 dnaJ+ gene.
gene that encodes a heat shock protein.";
J. Blol. Chem. 261:1782-1785(1986).
                                                                                          .;
0
                                Length 372;
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MEDLINE=86111849; PubMed=3003084;
Ohki M., Tamura F., Nishimura S., Uchida H.;
Nucleotide sequence of the Escherichia coli dnaJ gene and purification of the gene product.";
J. Biol. Chem. 261:1778-1781(1986).
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                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1998 (Rel. 08, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Chaperone protein dnaJ (Heat shock protein J) (HSP40).
Name-dnaJ; Synonyms-groP; OrderedLocusNames-b0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 88:2874-2878(1991).
                            100.0%; Score 86; DB 2; I
100.0%; Pred. No. 2.7e-06;
                                                                                                                                                                                                                                                                                                                                                                           375 AA.
                                                                                          0; Mismatches
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Nucleic Acids Res. 20:3305-3308(1992).
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                                                                                                                                                       1 QKRAAYDQYGHAAFEQ 16
                                                                                                                                                                                                             61 OKRAAYDOYGHAAFEO 76
                                                   Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli
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                                                                                                                                                                                                                                                                          RESULT 2
DNAJ_ECOLI
ID DNAJ_ECOLI
PO8622;
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                                   Query Match
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                       MEDIINE=2031465; PubMed=10891270; DOI=10.1006/jmbi.2000.3923;
Martinez-Yamout M., Legge G.B., Zhang O., Wright P.E., Dyson H.J.;
"Solution structure of the cysteine-rich domain of the Escherichia
coli chaperone protein DnaJ ";
J. Mol. Biol. 300:805-818(2000).
-! FUNCTION: Interacte with dnaK to disassemble a protein complex at
the phage lambda origin of replication. Stimulates, jointly with
grpk, the ATPASE activity of dnaK.
-! COPACTOR: Binds 2 zinc ions per monomer.
-! SUBUNIT: Homodimer.
-! SUBCELLULAR LOCATION: Cytoplasmic.
-! SUBCELLULAR LOCATION: Cytoplasmic.
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MEDLINE-99224904; PubMed-10210198;
Huang K., Flanagan J.M., Prestegard J.H.;
"The influence of C-terminal extension on the structure of the 'J-domain' in E. coli DnaJ.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gly-rich.
CXXCXGXG motif.
CXXCXGXG motif.
CXXCXGXG motif.
CXXCXGXG motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1. SIMILARITY: Belongs to the dnaJ family.
-1. SIMILARITY: Contains 1 CR domain.
-1. SIMILARITY: Contains 1 J domain.
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InterPro; IPR002393; DnaJ.C.
InterPro; IPR001305; DnaJ.CXXXXXXXXI
InterPro; IPR001305; DnaJ.CXXXXXXXI
InterPro; IPR003095; HSP DnaJ.
InterPro; IPR01031; Hultinaem_cyt.
Pfam; PF00286; DnaJ; 1.
Pfam; PF00586; DnaJ; 1.
Pfam; PF00685; DnaJ; 1.
Pfam; PR00625; DnaJ; 1.
PRNST; SM0021; DnaJ; 1.
PROSTIE; PS00637; DNAJ_1; 1.
PROSTIE; PS00637; DNAJ_2; 1.
PROSTIE; PS00637; DNAJ_2; 1.
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1BQ2; NWR; @=1-77.

1EXK; NWR; A=130-208.

1XBL; NWR; A=1-107.

DBASE; H036.5; 6TH EDITION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M12544; AAA00009.1; -.
EMBL; M12565; AAA23693.1; -.
EMBL; D10481; BAB96590.1; -.
EMBL; U00096; AAC73126.1; -.
PIR; A92572; HHSCDJ.
PDB; 1BQO; NMR; @=1-103.
                                                                                                                  Protein Sci. 8:203-214(1999).
                                                                                                                                                                           STRUCTURE BY NMR OF 130-208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ECO2DBASE; H036.5; 6TH 1
EchoBASE; EB0236; -.
EcoGene; EG10240; dnaJ.
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MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              From the formal of the following the following of the following of the following the following of the following following the following following the following 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 376 AA; 41072 MW; 1B354AC3F9844532 CRC64;
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GO; GO:0006260; P:DNA replication; IEA.
GO; GO:0006457; P:protein folding; IEA.
GO; GO:0006986; P:response to unfolded protein; IEA.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                     InterPro; IPR002939; Dnad_C.
InterPro; IPR01305; Dnad_C.XCXGGG.
InterPro; IPR001623; Dnad_N.
InterPro; IPR001623; Dnad_N.
InterPro; IPR001623; Dnad_N.
Pfam; PP00226; Dnad_C; 1.
Pfam; PP00684; Dnad_C; 1.
SMART; SM00271; Dnad_C; 1.
PROSITE; PS00199; CYTOCHROME C; UNKNOWN_2.
PROSITE; PS00636; DNAJ_1; 1.
PROSITE; PS00637; DNAJ_2; 1.
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Pfam; PF00684; DnaJ_CXXXXXXX; 1.
PRINTS; PR00625; DNAJPROTEIN.
PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chaperone protein dnaJ. Name=dnaJ; OrderedLocusNames=c0020;
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       InterPro; IPR000345; CytC_heme_BS.
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NCBI_TaxID=217992;
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Best Local Similarity 100.0%;

Matches 16; Conservative 0
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X MEDLINE-22590274; PubMed=12704152;

DOI=10.1128/IAI.71.5.2775-2786.2003;

Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,

A Wei J., Goldberg G.F., Plunkett G. III, Rose D.J., Darling A.,

A Muu B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,

Schwartz D.C., Blattner F.R.;

T "Complete genome sequence and comparative genomics of Shigella

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Bacteria; Flexneria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0RT-2004 (TrEMBLrel. 26, Last annotation update)
Chaperone with DnaK; heat shock protein.
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Zinc 2.
Zinc 1.
Zinc 1.
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Matches 16; Conservative
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STRAND SEQUENCE Query Match

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MEDLINE-21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H., Schoplete genome sequence of enterchemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

STRAIN=0157:H7 / EDL933 / ATCC 700927 / EHEC;

MEDLINE=21074355; bubmed=11206551; DOI=10.1038/35054089;

MEDLINE=21074355; bubmed=11206551; DOI=10.1038/35054089;

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Kink S., Boutin A., Shao Y., Miller L., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Melch R.A., Blattner F.R.;

"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";

Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bscherichia coli O157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                          100.0%; Score 86; DB 2; Length 376; 100.0%; Pred. No. 2.8e-06; Live 0; Mismatches 0; Indels
PROSITE; PS00636; DNAJ_1; 1.
PROSITE; PS50076; DNAJ_2; 1.
PROSITE; PS00637; DNAJ_CXXXXXXX CX.
Chaperone; Complete proteome; DNA replication; Heat shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Chaperone with DnaK; heat shock protein (DnaJ protein).
Name=dnaJ; OrderedLocusNames=BCS0015, 20015;
                                                                                        Chaperone; Complete proteome; DNA replication; Heat sh
Metal-binding; Repeat; Zinc.
SEQUENCE 376 AA; 41044 MW; 8B7ADC315B7E6F4A CRC64;
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GO:0006280; F:DNA replication; IEA.
GO:0006457; F:protein folding; IEA.
GO:0006986; P:response to unfolded protein; IEA.
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InterPro; IPR001503; Dnad_N.
InterPro; IPR008971; HSP40_Dnad_Dep
InterPro; IPR003095; HSp_Dnad_.
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InterPro; IPR002939; DnaJ_C.
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NCBI_TaxID=83334;
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                                                                                                                                                                                                                                         Local Similarity 100.
1es 16; Conservative
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                                                                                                                                                                                                                Query Match
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OBAA65

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DIT 01-M

DIT 25-0

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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STRAIN=3500HP / ATCC 700724;

A MUNISON RS. JT. Ray W.C., Mahairas G., Sabo P., Mungur R.,

Johnson L., Nguyen D., Wang J., Forst C., Hood L.;

"The complete genome sequence of Haemophilus ducreyi.";

"I have a co-chaperone. Stimulates, jointly with grpE,

"I FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,

"I FUNCTION: Acts as a co-chaperone. Stimulatity).

"I COFACTOR: Binds 2 zinc ions per monomer (By similarity).

"I SIMILARITY: Concains to the dnaJ family.

"I SIMILARITY: Concains 1 J domain.
                                                                                                                         PROSITE; PS00190; CYTOCHROME C; UNKNOWN 2.
PROSITE; PS00636; DNAJ 1; 1.
PROSITE; PS50076; DNAJ 2; 1.
PROSITE; PS00637; DNAJ CXXCXCXGXG; 1.
CARDFORD; DNA replication; Heat shock; Metal-binding; Repeat; Zinc; Complete proteome.
SEQUENCE 376 AA; 41044 MW; 8B7ADC315B7E6F4A CRC64;
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Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                     Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Parsons L.M.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 86; DB 2; I
100.0%; Pred. No. 2.8e-06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-mperone protein dnaJ.
Name=dnaJ; OrderedLocusNames=HD0188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              377 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001623; DnaJN.
InterPro; IPR008971; HSP40_DnaJ_Dep.
InterPro; IPR003095; HSP_DnaJ.
InterPro; IPR011031; Multinaem_cyt.
Pfam; PF00226; DnaJ; 1.
Pfam; PF01556; DnaJ_C; 1.
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Interpro; IPR001305; DnaJ CXXCXGXG.
Pfam; PF01556; DnaJ C; 1.
Pfam; PF00684; DnaJ CxXCXCXG; 1.
PRINTS; PR00625; DNAJPROTEIN.
SMART; SM00271; DnaJ; 1.
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STRAIN=35000HP / ATCC 700724;
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Query Match

Best Local Similarity 100.vv.,

Local 16; Conservative
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DNAJ HAEDU
ID DNAJ HAEDU
AC P48208;
   S K K K B D R B D R K K K K B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B D R B 
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378 AA;
Quail M.A., F
Whitehead S.,
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SEQUENCE
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SPECIES=S.typhi; STRAIN=CT18;
SPECIES=S.typhi; STRAIN=CT18;
MEDLINE=21534947; Pubmed=11677608; DOI=10.1038/35101607;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basaham D., Brooks R., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIBLE-S. Typhimurium, STRAIN-LT2 / SGSC1412 / ATCC 700720;
MEDLINE-21534948; PubMed=11677609; DOI=10.1018/35101614;
MCC1ellland M., Sanderson K.E., Szideth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Florae L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.;
Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Enterobacteriaceae, Salmonella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 86; DB 1; Length 377; 100.0%; Pred. No. 2.8e-06;
                          PRINTS; PRO0625; DNAJPROTEIN,
PROSITE; PS00636; DNAJ_1; 1.
PROSITE; PS00637; DNAJ_2; 1.
PROSITE; PS00637; DNAJ_CXXCXGXG; 1.
Chaperone; Complete proteome; DNA replication; Heat shock; Metal-binding; Repeat; Zinc.
                                                                                                                                                                                                                                                                                                                                                                        Zinc 1 (By similarity).
Zinc 1 (By similarity).
Zinc 2 (By similarity).
Zinc 2 (By similarity).
Zinc 2 (By similarity).
Zinc 2 (By similarity).
Zinc 1 (By similarity).
Zinc 1 (By similarity).
Zinc 1 (By similarity).
A; 37E9048F81A1A7A9 CRC64;
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Stephen R.J., Hinton J.C.D.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Chapperone protein dnaJ.
Name-dnaJ; OrderedLocusNames=STM0013, STY0013, t0013;
Salmonella typhimurium, and
                                                                                                                                                                                                    J-domain.
Gly-rich.
CXXCXGXG motif.
CXXCXGXG motif.
CXXCXGXG motif.
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        Pfam; PF00684; DnaJ CXXCXGXG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41027 MW;
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Les 16; Conservative
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189
200
203
377 AA;
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Q60004;
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METAL
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METAL
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                               SECUENCE FROM N.A.
SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644564;
DOI=10.1128/JB1.185.7.2330-2337.2003;
DON W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Bacteriol. 185:2330-2337(2003).

-!- FUNCTION: Interacts with dnaK to disassemble a protein complex at the phage lambda origin of replication. Stimulates, jointly with grpE, the ArPase activity of dnaK.

-!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).

-!- SUBGELLULAR LOCATION: Cytoplasmity.

-!- INDUCTION: By heat shock under the control of the htpR regulatory
                            Whitehead S., Barrell B.G.; "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18."; "Nature 413:848-852(2001).
M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DR InterPro; IPR001239; DnaJ_C.
DR InterPro; IPR001239; DnaJ_C.XCXCXGXG.
DR InterPro; IPR001301; HSP40_DnaJ_C.
DR InterPro; IPR001301; HSP40_DnaJ_Dep.
DR InterPro; IPR01031; HSP40_DnaJ_Dep.
DR InterPro; IPR01031; HSP40_DnaJ_Dep.
DR Fam; PF00126; DnaJ; 1.
DR Pfam; PF00126; DnaJ; 1.
DR Pfam; PF00126; DnaJ; 1.
DR Pfam; PF00126; DnaJ_CXXCXGXG, 1.
SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00036; DNAJ_1; 1.
DR PROSITE; PS00036; DNAJ_1; 1.
DR PROSITE; PS00037; DNAJ_1; 1.
DR PROSITE; PS00037; DNAJ_2; 1.
DR PROSITE; PS00037; DNAJ_2; 1.
DR PROSITE; PS00037; DNAJ_1; 1.
DR PROSITE; PS00037; DNAJ_1; 1.
DRAIN CAMPER PROFECE PROFECE
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Gly-rich.
CXXCXGXG motif.
CXXCXGXG motif.
CXXCXGXG motif.
CXXCXGXG motif.
CXXCXGXG motif.
Zinc 1 (By similarity).
Zinc 2 (By similarity).
Zinc 1 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein (By similarity).
--- SIMILARITY: Belongs to the dnaJ family.
--- SIMILARITY: Contains 1 CR domain.
--- SIMILARITY: Contains 1 J domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, US8360; AAB02911.1; -.
EMBL, AE008693; AAL18977.1; -.
EMBL, AL677265; CAD01166.1; -.
EMBL, AE016834; AA067747.1; -.
HSSP; P08622; 1EXK.
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CRC64

41181 MW;

ОВГЗДЗ

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Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O., Regala W.W., Georgescu A.M., Vergez L.M., Land M.L., Motin L.V., Begala W.W., Georgescu A.M., Vergez L.M., Land M.L., Motin L.V., Brubaker R.R., Fowler J., Hinnebusch B.J., Marceau M., Medigue C., Stionet M., Chenal-Francisque V., Souza B., Dacheux D., Elliott J.M., Darbise A., Hauser L.J., Garcia E.;

"Insights into the genome evolution of Yersinia pestis through whole genome comparison with Yersinia pseudotuberculosis.";

"Insights into the genome evolution of Yersinia pestis through whole T. FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE, the Transity of dnak (By similarity).

"In ATPASS activity of dnak (By similarity).

"SUGCELLULAR LOCATION: Cytoplasmic (By similarity).

"SUGCELLULAR Belongs to the dnaJ family.

"SUGCELLULAR PARISSES 11; P: PERPORGE to the dnaJ family.

"GO: GO:0006986; P: P: PERPORGE to unfolded protein; IEA.
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STRAIN=CO-92 / Biovar Orientalis;

STRAIN=CO-92 / Biovar Orientalis;

MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;

Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

Prentice M.B., Sebaihia M., James K.D., Churcher C.M., Mungall K.L.,

Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Peltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,

Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

"Genome sequence of Versinia pestis, the causative agent of plague.";

Nature 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8ZIM6; Q74Q12; Q7CG76; 01-WAR-2002 (TrEMBLrel. 20, Created) 01-WAR-2002 (TrEMBLrel. 20, Last sequence update) 25-CCT-2004 (TrEMBLRel. 28, Last annotation update) Chaperone protein DnaJ (Chaperone with DnaK; heat shock protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 86; DB 2; 1
Pred. No. 2.8e-06;
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100.0%; Pred. No. 4.-
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OrderedLocusNames=YP3711, YP00469, y3705;
                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002339; DnaJ C.
InterPro; IPR001305; DnaJ C.XCXGXG.
InterPro; IPR001871; HSP40_DnaJ Dep.
InterPro; IPR001871; HSP40_DnaJ Dep.
InterPro; IPR0011031; Multinaem_cyt.
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Pfam; PF01556; Dnad; 1.
Pfam; PF01556; Dnad C; 1.
PRINTS; PR00684; Dnad CXXCXGXG; 1.
PRINTS; PR00625; DNAJPROTEIN.
SWART; SM00271; Dnad; 1.
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Best Local Similarity 100.0
Matches 16, Conservative
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Q8ZIM6
RAY KAYAYA KAYAYA KAYAYA KAYAYAYA KAYAYA KAYAYA
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                                                            Gaps
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Yersinia pseudotuberculosis IP 32953.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
                                                                                                                                                                                                                                                                                                                                                                                          Colwellia maris (Vibrio sp. (strain ABE-1)).
Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Colwelliaceae; Colwellia.
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Heat shock protein, DnaJ and GrpB stimulates ATPase activity
             100.0%; Score 86; DB 1; Length 378; 100.0%; Pred. No. 2.8e-06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 86; DB 2; Length 379;
; Pred. No. 2.8e-06;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamauchi S., Okuyama H., Nishiyama Y., Hayashi H.; Submirted (ARR-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AB094455; BAB91324.2; -. HSSP; P08622; 1BQZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO: 0001082; F: unfolded protein binding; IEA.
GO; GO: 0001082; F: unfolded protein binding; IEA.
GO; GO: 0006986; P: response to unfolded protein; IEA.
InterPro; IPR000345; Cytc, heme_BS.
InterPro; IPR000345; Cytc, heme_BS.
InterPro; IPR001305; Dnad_CXXCXCXGG.
InterPro; IPR0018971; HSP40_DnaJ_pep.
Pfam; PF00126; Dnad; N.
Pfam; PF00126; Dnad; C.
I.
PROSITE; PS00190; CYTOCHROME C; UNKNOWN_I.
PROSITE; PS00636; DNAJ_I; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         379 AA; 40995 MW; 58A2894D13F8E9FA CRC64;
                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                         379 AA
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                                                                                                                                                                                                                                                                                                   Created)
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PROSITE; PS00637; DNAJ_CXXCXGXG; 1.
                                                                                                                                                                                                                                                         PRT;
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                                                                                                    1 OKRAAYDOYGHAAFEQ 16
                                                                                                                                              60 OKRAAYDOYGHAAFEO 75
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                                                                                                                                                                                                                                                                                          01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2003 (TrEMBLrel. 25,
01-MAR-2004 (TrEMBLrel. 26,
        Query Match
Best Local Similarity 100.
Matches 16; Conservative
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Best Local Similarity 100.'
Matches 16; Conservative
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                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                               Heat shock protein 40.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                   Name=dnaJ;
                                                                                                                                                                                                                                                                             QBL3D3;
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Gaps

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SEQUENCE FROM N.A

NCBI\_TaxID=273123; [1] SEQUENCE FROM N.A.

DnaK. RESULT 9
266ES9
1D 266E
AC 266E
DT 25-0
DT 25-0
DE Heat
DE DARW
GN Name
OS Yers
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Length 379;

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Science 269:496-512(1995).
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Les 16; Conservative
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P43735;
                                                                                                                                                  Eactors."
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Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
Perna N.T., Rose D.J., Mau B., Schwartz D.C.,
Fetherston J.D., Lindler L.E., Brubaker R.R., Planc G.V.,
Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
"Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).
                                                                                                                                                                                                                                                                                                                                                      STRAIN=91001 / Biovar Mediaevalis;
Song Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D.,
Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,
Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,
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PubMed=12563089; DOI=10.1073/pnas.0402424101;
Bell K.S., Sebaihia M., Pritchard L., Holden M.T.G., Hyman L.J.,
Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pectobacterium.
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Pfam, PF00226; DnaJ; 1.

Pfam, PF00226; DnaJ; 1.

Pfam, PF0064; DnaJ; 1.

PRINTS; PR00625; DnaJ; 1.

PROSITE; PS00619; CYTOCHROME_C; UNKNOWN_2.

PROSITE; PS0076; DNAJ_2; 1.

PROSITE; PS00637; DNAJ_2; 1.

PROSITE; PS00637; DNAJ_2; 1.

RAJELANDER PROSITE; PS00637; DNAJ_2; 1.

REQUENCE 319 AA; 41278 MW; AC1922FC3D707C93 CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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Name=dnaJ; OrderedLocusNames=ECA3881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
STRAIN=KIM5 / Biovar Mediaevalis;
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06008
AC 06008
DT 25-0C
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   SO KKE BODD BROWN BODD BROWN B
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Whole-genome random sequencing and assembly of Haemophilus influenzae
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-!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE, the Arpsas activity of dank (By similarity).

-!- COPACTOR: Binds 2 zinc jons per monomer (By similarity).

-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

-!- SIMILARITY: Belongs to the dnaJ family.

EMBL; BX950851; CAG767791.1; --

GO; GO:0051082; F:unfolded protein binding; IEA.

GO; GO:0006457; P:protein folding; IEA.

InterPro; IPR000045; CytC_heme_BS.
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Pleischmann R.D., Addam M.D., White O., Clayton R.A., Kirkness E.F.,
Fleischmann R.D., Addam M.D., White O., Clayton R.A., Merrick J.M.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G.G., FitzHugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Witerback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
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Pasteurellaceae, Haemophilus.
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SEQUENCE 379 AA; 41212 MW; 3814B164D55F8CB9 CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Chaperone protein dnaJ.
Name=dnaJ; OrderedLocusNames=H11238;
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InterPro; IPR001309; Dnad_CXCXCXGG.
InterPro; IPR001623; Dnad_N.
InterPro; IPR008971; HSP40_Dnad_pep.
InterPro; IPR0103095; HSp Dnad.
InterPro; IPR011031; Multihaem_Cyt.
Pfam; PP00226; Dnad; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01556; Dnad_C; 1.
Pfam; PF000684; Dnad_CXXCXGXG; 1.
PRINTS; PR00625; DNAJPROTEIN.
SMART; SM00271; Dnad; 1.
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"Genome sequence of Shigella flexneri 2a: insights into pathogenicity
"Genome sequence of Shigella flexneri 2a: insights into pathogenicity
"Through comparison with genomes of Escherichia coli K12 and 0157.";
"Uncleic Acids Res. 30:4432-4441(2002).
"L'EUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE,
the ATPBRS activity of dnaK (By similarity).
"C -!- COPACTOR: Binds 2 zinc ions per monomer (By similarity).
"C -!- SIMILARITY: Belongs to the dnaJ family.
"REMBL; AE015039; AAN41681.1; -..
RSSP; PO8622; IEXK.
"R GO; GO:00051082; Funfolded protein binding; IEA.
"R GO; GO:0006508; P:INA replication; IEA.
"R GO; GO:0006508; P:response to unfolded protein; IEA.
"R GO; GO:0006586; P:response to unfolded protein; IEA.
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MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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Pasteurellaceae, Actinobacillus.
NCBL_TaxID=714,
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SEQUENCE 386 AA; 42279 MW; 172BC403A6E7D75E CRC64;
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100.0%; Pred. No. 2.8e-06;
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30-MAY-2000 (Rel. 39, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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tes 16; Conservative
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P77866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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DNAJ_ACTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
 8
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                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpE, the ATPase activity of dnaK (By similarity).
COFACTOR: Binds 2 zinc ions per monomer (By similarity).
SUBCELLULIAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to the dnaJ family.
SIMILARITY: Contains 1 CR domain.
SIMILARITY: Contains 1 J domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
NCBI_TaxID=623;
[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00636; DNAJ_1; 1.
PROSITE; PS000616; DNAJ_2; 1.
PROSITE; PS00037; DNAJ_CXXCXGXG; 1.
Chaperone; Complete proteome; DNA replication; Heat shock;
Metal-binding; Repeat; Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zinc 2 (By similarity).
Zinc 2 (By similarity).
Zinc 2 (By similarity).
Zinc 1 (By similarity).
Zinc 1 (By similarity).
Zinc 1 (By similarity).
8850B88B6FBZBCZB CRC64;
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Zinc 2 (By similarity).
Zinc 1 (By similarity).
Zinc 1 (By similarity).
Zinc 1 (By similarity).
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
Chaperone with DnaK; heat shock protein.
Name-dnaJ; OrderedLocusNames=SF0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 86; DB 1; I
100.0%; Pred. No. 2.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gly-rich.
CXXCXGXG motif.
CXXCXGXG motif.
CXXCXGXG motif.
CXXCXGXG motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 386 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J-domain.
                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001939; DnaJ C.
InterPro; IPR001305; DnaJ_CXXCXGXG.
InterPro; IPR001623; DnaJ N.
InterPro; IPR001095; Hsp DnaJ.
InterPro; IPR0101091; Multihaem_cyt.
Pfam; PF00226; DnaJ; 1.
Pfam; PF00684; DnaJ CXXCXGXG; 1.
Pfam; PF00684; DnaJ_CXXCXGXG; 1.
PRINTS; PR00685; DNAJPROTEIN.
                                                                                                                                                                                                                                                                                                 EMBL; U32803; AAC22890.1; ALT_INIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
ses 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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203
382 AA;
                                                                                                                                                                                                                                                                                                                                            HI1238
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Q83MH4;
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REPEAT
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DOMAIN

rigr;

REPEAT

Best Loca Matches

δ g RESULT 13
083MH4
AC 083MH
AC 083MH
DT 01-JU
DT 01-JU
DT 01-MA
DE Chape
GN Shige
OC Bacte
OC Bacte
OC NCBI

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Gaps

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Length 386;

us-10-001-938-3.open.rup

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Search completed: March
Job time : 67.5894 secs
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Metal-binding;
                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                   Putative DnaJ protein, DnaJ-class molecular chaperone with C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
the ATPase activity of dnak (By similarity).
COFACTOR: Binds 2 zinc ions per monomer (By similarity).
SUBSCLIGULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to the dnaJ family.
SIMILARITY: Contains 1 CR domain.
SIMILARITY: Contains 1 J domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=ECS0015; OrderedLocusNames=PBPRA0698;
Photobacterium profundum (Photobacterium sp. (strain SS9)).
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Photobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96.5%; Score 83; DB 1; Length 375; 93.8%; Pred. No. 9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CF9D286756FF44E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     Zinc 1 (By Similarity).
Zinc 1 (By Similarity).
Zinc 2 (By Similarity).
Zinc 2 (By Similarity).
Zinc 2 (By Similarity).
Zinc 2 (By Similarity).
Zinc 1 (By Similarity).
Zinc 1 (By Similarity).
Zinc 1 (By Similarity).
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                            CXXCXGXG motif. CXXCXGXG motif. CXXCXGXG motif.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                        J-domain.
Gly-rich.
                                                                                                                                                                                                                                                                                                                                                                                                             CXXCXGXG
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                                                                                                                                                                  EMBL; D87753; BAA32697.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKRAAYDOYGHAAFEO 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 93.8 tes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             375 AA;
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                                                                                                                                                                               P08622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                               REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
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06LUA
AC 06LUA
AC 06LUA
DT 05-JU
DT 05-JU
DE PLIAT
DE PLIAT
DE NAME
CO PROTO
OC PROTO
OX NOBI
RN (CI)
RP (CI)
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7, 2005, 07:52:39

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                                                                                                                                      high pressure adaptations. "I submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.

Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.

-- FUNCTION: Acts as a co-chapperone. Stimulates, jointly with grpE, the ArPase activity of dama (By similarity).

-- COFACTOR: Binds 2 zinc ions per monomer (By similarity).

-- SIMILARITY: Belongs to the dnaJ family.

-- SIMILARITY: Belongs to the dnaJ family.

R GO, GO:0001002; F:unfolded protein binding; IEA.

R GO, GO:0001002; F:unfolded protein binding; IEA.

R GO, GO:0006457; P:protein folding; IEA.

R InterPro; IPR001305; DnaJ C.

R InterPro; IPR001305; DnaJ C.

R InterPro; IPR001305; DnaJ C.

R Ffam; PF0026; DnaJ; 1.

R Pfam; PF0026; DnaJ; 1.

R Pfam; PR00262; DnaJ; 1.

R Pfam; PR00684; DnaJ CXXCXGKG; 1.

R Pfam; PR00685; DNaJ CXXCKKGK; 1.

R Pfam; PR00685; DNaJ CXXCKKGK; 1.

R Pfam; PR00685; DNaJ CXXCKKKG; 1.

R Pfam; PR00685; DNaJ CXXCKKGK; 1.

R PRINTS; RR00625; DNAJ CXXCKKGK; 1.
                                                                                                                  ĕ
Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F., Cestaro A., Malacrida G., Simionati B., Cannata N., Bartlett D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                              Genome analysis of Photobacterium profundum reveals the complexity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
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PROSITE; PS00636; DNAJ 1; 1.
PROSITE; PS50076; DNAJ 2; 1.
PROSITE; PS00637; DNAJ 2XXXXXXX 1.
Chaperone; Complete proteome; DNA replication; Heat shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 96.5%; Score 83; DB 2; Length 380; Best Local Similarity 93.8%; Pred. No. 9.1e-06; Matches 15; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40802 MW; 772DD9F069899B63 CRC64;
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ng sw model	March 7, 2005, 07:13:17; Search time 77.9868 Seconds (without alignments) 79.349 Million cell updates/sec
usin	05, 0
arch,	7, 20
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OM protein	Run on:
	OM protein - protein search, using sw model

2105692 seqs, 386760381 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 1 OKRAAYDQYGHAAFEQ 16 US-10-001-938-3 86 Perfect score: Scoring table: Sequence: Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* A\_Geneseq\_16Dec04:\* geneseqp1980s:\* Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STRAMMIS

	Description	Aau98852 E.Coli DN	Abr55126 E. coli d	Aab11396 E. coli e	Aab74197 OmpA-J do					Aaul7587 Novel sig	Adb94295 Human nov		Adr89339 E. coli p	Adn18036 Bacterial	Adn17733 Bacterial	Ads42875 Bacterial	Adf05627 Bacterial			Aab74196 OmpA-DnaJ	Aab70766 Expressio	Aay72017 E. coli O	Abg1771 Novel hum	Per	Aay79543 E. coli d	Aam99341 Vaccine r
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SUMMAKIES	ID	AAU98852	ABR55126	AAB11396	AAB74197	AAB70767	AAY72018	AAU17588	ADB94296	AAU17587	ADB94295	ABM67485	ADR89339	ADN18036	ADN17733	ADS42875	ADF05627	ABO62494	AAB11395	AAB74196	AAB70766	AAY72017	ABG17771	AAW25795	AAY79543	AAM99341
	DB	5		m		4	4	4	7	•		9	œ		œ	œ		7	m	4	•	4	4	~	m	4
	Length	16	16	131	131	131	131	340	340	341	341	373	376	376	378	378	380	380	399	399	399	399	476	15	15	15
de	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	94.2	94.2	94.2
	Score	98	98	98	98	98	98	98	98	98	98	98	98	98	98	98	98	98	98	86	86	98	86	81	81	81
	Result No.	п	7	m	4	S	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Aau09842 B.coli dn Aau9876 E. coli D Aac19457 Human hea Abr55132 E. coli D Aam99344 Vaccine r Aau02075 Synthetic Aau02075 Synthetic Ada21615 Bacterial Ad821615 Bacterial Ad823054 Bacterial Abp80877 N. gonorr Aar95446 RA suscep Aav2546 Peptide d Aaw25796 Peptide d Aaw25513 B. coli d Adn2513 B. coli d Adn2512 Bacterial	Adr31368 Stress re Adn24677 Bacterial Adn21920 Bacterial Aar95445 RA suscep
AAU09842 AAU98876 AAE19457 AAB55132 AAM93344 AAU02075 AAU02077 AADS21615 ADS23054 AAP896477 AAR96477 AAR95133 AAR55133 ABR55133 ABR55133	ADR31368 ADN24677 ADN21920 AAR95445
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24 24 24 24 24 24 24 24 24 24 24 24 24 2	376 379 380
44444444666666666666666666666666666666	77.9 77.9 77.9
88111427777337788811147727777	67 67 64.5
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	4 4 4 4 C1 62 4 70

## ALIGNMENTS

RESULT 1

Immunogenic peptide; heat shock protein; HSP; DNAJ; immunomodulatory; cytostatic; antiinflammatory; antibacterial; antiarthritic; autoimmune disease; arthritis; articular juvenile idiopathic arthritis; infectious disease; inflammatory bowel disease; cancer; mucosal tolerisation; DNA vaccination; anergy induction. E.Coli DNAJ 61 immunogenic peptide. AAU98852 standard; peptide; 16 AA. (first entry) 22-AUG-2002 AAU98852; AAU98852 

Escherichia coli.

WO200236611-A2. 10-MAY-2002. 31-OCT-2001; 2001WO-US045344.

01-NOV-2000; 2000US-0245181P.

(REGC ) UNIV CALIFORNIA. (MART/) MARTINI A.

Carson DA, Martini A, Albani S,

Prakken BJ;

New immunomodulatory peptides from heat shock proteins, useful for treating immunological disorder in subjects such as humans, e.g. autoimmune disease (e.g. arthritis), infectious disease, inflammatory bowel disease or cancer. WPI; 2002-489999/52.

Claim 4; Page 55; 84pp; English.

This invention relates to the use of a peptide, which is an immunogenic portion derived from a dnaj heat shock protein (hsp) in modulating an immune response in a subject. The peptides of the invention may have immunomodulatory, cytostatic, antiinflammatory, antibacterial or antiarthritic properties and can stimulate expression of interleukins, tumour necrosis factor and transforming growth factor better. The immunogenic peptide is useful for modulating (i.e. augmenting) inducing or reducing/inhibiting) an immune response in a subject having an

invention

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel method for modulating an immune response in a subject having an immune-related disorder. The method comprises: (a) administering an antigen-specific epitope, where administration provides epitope-specific T cell immune modulation; and (b) administering a cytokine, an agent that effects cytokine activity or expression, or an anticytokine therapy. The method of the invention has antiarthritic, antidiabetic, neuroprotective, anti-inflammatory, cytostatic, anti-asthmatic, anti-inflammatory, cytostatic, anti-uncer, antianaemic, cardiant, respiratory general, antiallergic, dermatological, and antipsoriatic activity. The method is useful for modulating an immune response in a subject having an immune-related disorder. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modulating an immune response in a subject having an immune-related disorder, e.g. arthritis by administering an antigen-specific epitope and a cytokine or an agent that effects cytokine activity or expression.
            articular juvenile idiopathic arthritis), an infectious disease, an inflammatory bowel disease or cancer. The immunogenic peptide of the invention is also useful for modulating immunosficetor cell responsiveness in a subject. The immunogenic peptide is particularly useful for treating the above-mentioned diseases in mammals, e.g. cat, dog, horse, farm animal (e.g. ovine, bovine or porcine) or human. In general, the peptide is useful in methods involving mucosal tolerisation, DNA vaccination, anergy induction or active immunisation. The present sequence represents an E. coli DNA immunogenic peptide of the invention
                                                                                                                                                                                                                                                                                                          Gaps
immunological disorder (e.g. autoimmune disease such as arthritis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antigen-specific epitope; immune response; T cell; cytokine; antiarthritic; antidiabetic; neuroprotective; anti-inflammatory; cytostatic; antithyroid; antischmatic; immunosuppressive; antipporiatic; anti-ulcer; antianaemic; cardiant; respiratory; antiallergic; dermatological; antipporiatic.
                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                    Length 16;
                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                    100.0%; Score 86; DB 5; I 100.0%; Pred. No. 4.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coli dnaJ61 antigen-specific epitope peptide.
                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 9; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABR55126 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-SEP-2001; 2001US-0325499P.
11-DEC-2001; 2001US-0339284P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-SEP-2002; 2002WO-US030578
                                                                                                                                                                                                                                                                                                                                                     16
                                                                                                                                                                                                                                                                                                                                                                                           OKRAAYDOYGHAAFEO 16
                                                                                                                                                                                                                                        Query Match
Query Match
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Local Similarity
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Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Martins A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-430097/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli
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                                                                                                                                                                                                                             Sequence 16 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABR55126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              naturally occurring enkaryotic polypeptide containing two or more cysteine units bound via a disulfide bridge which comprises cultivation of prokaryotic cells in the presence of arginine or an amide compound. The method is useful for the proparation of eukaryotic proteins e.g. proteases, interferons, protein hormones, antibodies or antibody fragments (e.g. a single chain FV fragment that binds to thyroid stimulating hormone). It is especially useful for preparing proteins with more than five disulfide bridges, e.g. recombinant plasminogen activator (rPA). The technique is simple and does not require in vitro aftertreatment, such as the removal of inclusion bodies, reduction or
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Preparation of water-soluble eukaryotic polypeptides with disulfide bridges e.g. rPA, comprises cultivation of prokaryotic cells in the presence of arginine or amide compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E. coli expression plasmid pUBS520-pIN-J-Domain encoded protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel preparation of a water-soluble,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryotic protein; protease; interferon; antibody; hormone;
disulfide bridge.
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                                                            Length 16;
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100.0%; Pred. No. 4.7e-07;
tive 0; Mismatches 0;
                                                                                      4.7e-08;
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                                                                   100.0%; Fr.
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                                                            100.08;
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                                                                                   Best_Local Similarity 100.
Matches 16; Conservative
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es 16; Conserv
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Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-APR-1999;
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Matches
                                                                                                                                                                                                                                                                                                                                      RESULT 3
                                                                                                                                                                                                                                                                                                                                                                   AAB11396
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This invention describes a novel method for preparing a naturally folded eukaryotic polypeptide (I) that contains two or more disulfide-bridged Cys residues by culturing prokaryotic cells that contain an expression vector for (I) including a prokaryotic signal sequence at its N-terminus and a nucleic acid (II) that secretes a chaperone protein (III) into the periphasm. (I) is secreted into the periplasm or medium, the signal peptide is then cleaved and (I) isolated from the periplasm or medium. The method is used for production of antibody, interferon, protein method is simple and eliminates time-consuming in vitro processing operations such as dissolution of inclusion bodies, reduction and refolding. (III) protects (I) against agglomeration and promotes their
                                                                                                                                                                                                                                                              Preparation of naturally folded eukaryotic proteins, e.g. antibodies, l
simultaneous expression of a chaperone protein, allows simple recovery
from periplasm or medium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E. coli OmpA-J domain fusion protein encoded by pUBS520-pIN-J-domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Secreted protein; chaperone; interferon; protease; hormone; fusion protein; naturally folded protein; lac-Ipp promoter; DnaJ; heat shock protein; HSP; outer membrane protein A; OmpA; J domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 131;
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Pred. No. 4.7e-07;
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                                                                                                                                                                         (HOFF ) HOFFMANN LA ROCHE & CO AG F.
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      natural conformation
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                                                                                                                                                                                                                                     N-PSDB; AAF61191
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                  EP1077263-A1.
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                                                                                               29-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a method for production of a naturally folded eukaryotic protein containing two or more cysteines linked by disulfide bridges. The method comprises co-expression and secretion into the periplasm of a molecular chaperone via an expression vector coding for the chaperone. The expression vector also encodes a signal sequence. The method is useful for producing a naturally folded eukaryotic protein such as an antibody, antibody fragment, interferon, protein hormone or a protease containing two or several cysteines linked by disulfide bridges.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Producing naturally folded eukaryotic proteins e.g. antibodies, interferon, hormones or proteases that contain two or several cysteines linked by disulfide bridges comprises co-expression of a molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a fusion protein composed of the OmpA signal sequence and the J domain of DnaJ. This sequence was used in the method
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                                                                                                                                                                         Molecular chaperone; OmpA signal sequence; J domain; DnaJ.
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                  AAB74197 standard; protein; 131 AA.
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                                                                                                                                    OmpA-J domain fusion protein.
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les 16; Conservative
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N-PSDB; AAF77804
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                                                                                                                                                                                                                                                      EP1077262-A1
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                                                                                               29-MAY-2001
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2000US-0231242P.
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2000US-0231968P.
2000US-0232397P.
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2000US-0237037P.
2000US-0237038P.
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                                                                                                                                                     07-JUN-2000;
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  The patent discloses a method for the production of a water-soluble, naturally folded and secreted eukaryotic proteins in prokaryotic cells. The method involves culturing the prokaryotic cells, containing an expression vector encoding the desired protein and the prokaryotic signal sequence, in the presence of an additive, e.g., L-arginine. The signal sequence mediates the secretion of the desired protein into the periplasm, where folding of the protein takes place. The prokaryotic cell also contains an expression vector encoding a molecular chaperone, e.g., DnaJ and haat shock protein 25 (HSPS5). The simultaneous co-oversypression and co-secretion of molecular chaperones in the periplasm improves the yield of functionally folded protein. The above method recombinantly produces a high yield of eukaryotic secreted proteins in provession and co-secretion of molecular chaperones in the protein such a sum antibody, antibody fragment, interferon, protein encoded by protease. The present sequence-J domain, fusion protein encoded by pubBS520-pIN-J-domain. The plasmid, pubBS520-pIN-J-domain.

Coff domain, which is the N-terminal portion of the DnaJ, facilitates the plasmid and position of the DnaJ, facilitates the
                                                                        Producing water-soluble, naturally folded, and secreted eukaryotic oblypeptide, involves culturing prokaryotic cells containing an expression vector encoding the polypeptide in the presence of arginine or a specific compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neuroprotective, cytostatic; dermatological; immunosuppressive; tumour; antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer; immune system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; chromosommal abnormality; Down syndrome; ischaemia; renal disorder; cardiovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AlDS; acquired immune deficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 86; DB 4; Length 131; 100.0%; Pred. No. 4.7e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel signal transduction pathway protein, Seq ID 1153.
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Best Local Similarity 100.6
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2001-033777/05.
                        N-PSDB; AAD02210.
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AAU17588
ID AAU1
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AAC AAU1
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DT 07-N
DT 07-N
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NW antimut
XW antimut
XW sick
XW chrc
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The invention relates to novel isolated polypeptides (I), and

C polynucleotides (II). (I), (II) and the antibody to (I) are useful for

C diagnosing, preventing and treating diseases including immune system

C disorders (e.g. congenital and acquired immunodeficiencies, autoimmune

C disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ

C disorders, primary haster versus host disease, infectious diseases

C (e.g. hepatitis C), bleeding disorders, hemoglobin abnormalities and

CC disorders, primary hasmatopoletic disorders, hyperporliferative disorders

CC disorders, primary hasmatopoletic disorders, hyperporliferative disorders

CC disorders, primary hasmatopoletic disorders, invomosomal abnormalities

CC disorders, primary hasmatopoletic disorders, cis stroke, renal disorders (e.g.

Alzheimer's disease, Parkinson's disease), chromosomal abnormalities

CC down syndrome), ischemic injury (e.g. stroke), renal disorders (e.g.

C pown syndrome), ischemic injury (e.g. stroke), renal disorders (e.g.

C glomerulonephritis), cardiovascular disorders (e.g. arrhythmia),

CC epithelal cell proliferation, endocrine disorders (e.g. Addison's

C disease), reproductive system disorders (cirrhosis), as stimulators of

C (inflammatory disorders), liver disorders (cirrhosis), as stimulators of

C (inflammatory disorders), liver disorders (cirrhosis), as stimulators of

C higher affinity antibodies, and as a means to induce tumour proliferation

C shundres of the invention

ANUTOSES

Gaps

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Query Match 100.0%; Score 86; DB 4; Length 340; Best Local Similarity 100.0%; Pred. No. 1.3e-06; Matches 16; Conservative 0; Mismatches 0; Indels

sequences of the invention

Claim 1; SEQ ID NO 1153; 880pp; English.

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Ruben SM;
                                                                                  01. NOV-2000; 2000US-0244617P.
08. NOV-2000; 2000US-0246474P.
08. NOV-2000; 2000US-0246476P.
08. NOV-2000; 2000US-0246476P.
08. NOV-2000; 2000US-0246477P.
08. NOV-2000; 2000US-0246524P.
08. NOV-2000; 2000US-024652P.
08. NOV-2000; 2000US-024652P.
08. NOV-2000; 2000US-024652P.
08. NOV-2000; 2000US-024651P.
08. NOV-2000; 2000US-024661P.
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2000US-0251856P
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human; autoimmune disease; Parkinson's disease; silicosis; gastrointestinal disease; atherosclerosis; haemophilia; thrombocytopenia; maunosophypressive agent; adjuvant; enhance immune response; higher affinity antibody induction; increased serum immunoglobulin concentration. ADB94296 standard; protein; 340 AA. 2000US-0179065P. 2000US-0180628P. 2000US-0214886P. 2000US-0216647P. 2000US-0216880P. 2000US-0217487P. 2000US-0217496P. 2000US-0220963P. 2000US-0220964P. 2000US-0224518P. 2000US-0218290P 17-JAN-2001; 2001US-00764868 2000US-0225268P 1 OKRAAYDOYGHAAFEO 16 2000US-0224519P 04-DEC-2003 (first entry) Human novel protein #530. US2002168711-A1. Homo sapiens 31-JAN-2000; 07-JUL-2000; 14-AUG-2000; 14-AUG-2000; 28-JUN-2000; 14-NOV-2002 ADB94296; ADB94296 ID ADB9 RESULT 셤 8

Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders.

WPI; 2001-465460/50. N-PSDB; AAS27505.

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R 14-ANG-2000; 2000US-2025477P.
R 14-ANG-2000; 2000US-2025787P.
R 14-ANG-2000; 2000US-2025787P.
R 14-ANG-2000; 2000US-2025787P.
R 14-ANG-2000; 2000US-2025787P.
R 14-ANG-2000; 2000US-2025788P.
R 10-SEP-2000; 2000US-202538P.
R 20-SEP-2000; 2000US-202
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the nucleic acid and the antibody are useful as immunosuppressive agents, as adjuvants to enhance immune responses, and as agents to induce higher affinity antibodies and increase serum immunoglobulin concentrations. The
                                            present sequence represents the amino acid sequence of a novel human protein. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format direct from USPTO at seqdata.uspto.gov/sequence.html?DocID=20020168711.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour;
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2000US-021513F
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2000US-0217497F
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2000US-0224518P.
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2000US-0205515P.
2000US-0209467P.
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2000US-0225268P
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                                                                                                                       Sequence 340 AA;
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19-MAY-2000;
07-JUN-2000;
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Matches
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AAU17587
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27-SEP-2000; 20000S-023-5836P.
29-SEP-2000; 20000S-023-6327P.
29-SEP-2000; 20000S-023-636P.
29-SEP-2000; 20000S-023-636P.
29-SEP-2000; 20000S-023-63F.
02-0CT-2000; 20000S-023-63F.
02-0CT-2000; 20000S-023-63F.
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2000US-0237040P
2000US-0239937P
2000US-0240960P
2000US-0241221P
2000US-0241785P
2000US-0241786P
2000US-0241786P
2000US-024186P
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2000US-0241809P
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2000US-0228924P.
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2000US-0246609P 2000US-0246610P 2000US-0246611P 2000US-0249207P 2000US-0249209P 2000US-0249209P 2000US-0249211P 2000US-0249211P 2000US-0249211P 2000US-0249211P 2000US-0249211P 2000US-0249211P 2000US-0249211P 2000US-0249299P. 2000US-0249300P. 2000US-0250160P. 2000US-0250391P. 2000US-0249217P. 2000US-0249218P. 2000US-0249244P. 2000US-0249245P 2001US-0259678P 08-NOV-2000; 08-NOV-2000; 08-NOV-2000; 17-NOV-2000; 05-DEC-2000; 05-DEC-2000; 05-DEC-2000; 08-DEC-2000; 05-JAN-2001; 17-NOV-2000; 17-NOV-2000; .7-NOV-2000; 17-NOV-2000; .7-NOV-2000; 17-NOV-2000; 01-DEC-2000; 17-NOV-2000; 01-DEC-2000 08-DEC-2000 

(HUMA-) HUMAN GENOME SCI INC

Ruben SM Rosen CA, Barash SC,

WPI; 2001-465460/50. N-PSDB; AAS27504.

Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders.

Claim 1; SEQ ID NO 1152; 880pp; English.

The invention relates to novel isolated polypeptides (1), and diagnosing, preventing and treating diseases including immune system diagnosing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune disorders (e.g. congenital and acquired immunodeficiencies, autoimmune clasorders (e.g. thepatitis), bleeding disorders, infections diseases (e.g. hepatitis C), bleeding disorders, nemegolobin abnormalities and other blood-related disorders (sickle cell anaemia), myeloproliferative disorders, primary haematopoletic disorders, primary haematopoletic disorders, primary haematopoletic disorders, increases, Parkinson's disease), chromosomal abnormalities (e.g. Gaucher's disease, Parkinson's disease), chromosomal abnormalities (c.g. Gaucher's disease, parkinson's disease), chromosomal abnormalities companies, ischemation's disease), chromosomal adisorders (e.g. alzhythmia), crespiratory disorders, dermatological disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders (e.g. arrhythmia), chematological disorders (e.g. arrhythmia), chiquent disorders (inflammatory disorders), liver disorders (cirrhosis), as stimulators of the B-cell responsiveness to pathogens, activators of T-cells, to induce (inflammatory disorders), and as a means to induce tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17059-AAU17683 represent novel signal transduction pathway protein, amino acid

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ABM67485 standard; protein; 373 AA.
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                                                   100.0%; Score 86; DB 4; Length 341;
100.0%; Pred. No. 1.3e-06;
iive 0; Mismatches 0; Indels
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sequences of the invention
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Best Local Similarity 100.
Matches 16; Conservative
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The invention relates to an isolated polypeptide. The polypeptide is useful for diagnosing a pathological condition or a susceptibility to a pathological condition in a subject, by determining the presence or amount of expression of the polypeptide in a biological sample and diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the polypeptide is also useful for identifying a binding partner to the polypeptide, which involves contacting the polypeptide or the polypeptide is useful for identifying a binding partner and determining whether the binding partner of the polypeptide is useful for preventing, treating, or analorating a medical condition, which involves administering the polypeptide or the nucleic acid to a mammalian subject. The nucleic acid condition in a subject, which involves determining the pathological condition in a subject, which involves determining the pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or absence of a mutation in the mutation. The polypeptide, the mucleic acid and an antibody to the polypeptide are useful for treating catch and an antibody to the polypeptide are useful for treating autonimmune disease, Parkinson's disease, silvestive to indice the indication of an antibody are useful as immunosuppressive agents, and all and an antibody are useful as immunosuppressive phyperical and an antibody are useful as immunosuppressive phyperical and an antipody are useful as immunosuppressive adents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as adjuvants to enhance immune responses, and as agents to induce higher affinity antibodies and increase serum immunoglobulin concentrations. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polypeptide useful for diagnosing and treating immunosuppressive conditions such as autoimmune disease and Parkinson's
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2000US-0241785P.
2000US-0241809P.
                                                                     2000US-0239935P.
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2000US-0251868P.
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Matches 16; Conservative
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N-PSDB; ADB93672.
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(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
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                                                             13-OCT-2000; 20-OCT-2000; 20-OC
                                                                                                                                                                                                                                                                                                    20-OCT-2000;
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PFRF; protein-folding-related factor; chaperone; GroES; GroEL; DnaK; DnaJ; GrpE; gene function; cell-free synthesis; recombinant protein production; therapeutic protein.

Escherichia coli

WO2004072107-A1

26-AUG-2004

E. coli protein-folding-related factor, DnaJ.

(first entry)

18-NOV-2004

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The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of P. luminescens and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polypeptides encoded by the genes are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that animals or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P. luminescens. Cells transformed to express the genes are useful for recombinant production of the proteins, particularly roxins and cells unsetul as insecticides, bartericides and fungicides. The genes, proteins, vectors containing the genes and Ab are also useful thrapacterials useful as insecticides, bacteria or fungir that are sensitive to P. luminescens-encoded toxins or antibiotics) and as biopesticides. Other uses of the genes and the proteins are as virulence in the containing the proteins or antibiotics) and as biopesticides. Other uses of the genes and the proteins are as virulence interperent and for identifying targets of human diseases for which P. Luminescens and for identifying targets of human diseases for which P.
                                                                                                                                    Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
                                                                                                                                                            detection, food, gene expression, plant; animal, microorganism; toxin, antibiotic; biopesticide; virulence factor; disease model; plague;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            luminescens is a model (particularly plague and whooping cough).sequence represents one of the isolated P. luminescens proteins
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                                                                                       Photorhabdus luminescens protein sequence #582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; SEQ ID NO 582; 1205pp; French.
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(CNRS ) CNRS CENT NAT RECH SCI
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                                             (first entry)
                                                                                                                                                                                                                                                 Photorhabdus luminescens
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Best Local Similarity
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                                                                                                                                                                                                         whooping cough.
                                                                                                                                                                                                                                                                                                 WO200294867-A2.
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                                             20-NOV-2003
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Producing soluble proteins using transformed genes encoding protein-folding-related factors in a cell-free protein synthesis system, useful in therapeutic, industrial and research purposes.

Example 1; SEQ ID NO 4; Sapp; English.

Lee KY;

Kim HJ, Jun SY,

Choi WJ,

Kang SH,

WPI; 2004-616042/59.

(DREA-) DREAMBIOGEN CO LTD.

13-FEB-2004; 2004WO-KR000302. 15-FEB-2003; 2003KR-00009628.

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reparing cells transformed by genes encoding protein-folding-related factors (PRR), so that the transformed cells can express enhanced levels of the PRRS, over-expressing the factors and preparing a cell extract cortaining the factors and preparing a cell extract producing a high level of soluble protein in the synthesis system from the transformed cells, and producing a soluble protein is one or more in number, and/or is a chaperone that is GroES/GroEL chaperone family or Dnak/Dnay/GrpE chaperone family. The cell extract is prepared from one or more transformed cells. The protein is alpha, beta, gamma-interferon, lipase, erythropoietin, cytokines, interleukins, granulocyte-colony stimulating factor, granulocyte macrophage-colony stimulating factor, transforming growth factors, thrombopoietin, or tissue plasminogen activator. The producing soluble proteins applicable to therapeutic, industrial and producing solubbe proteins applicable to therapeutic, industrial and research purposes, in particular for assaying functions of newly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           research purposes, in particular for assaying functions of newly discovered genes. The present sequence represents the amino acid sequence of an E. coli DnaJ, a protein-folding-related factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to producing soluble protein. The method involves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
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OKRAAYDQYGHAAFEQ 16 OKRAAYDOYGHAAFEO 76

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RESULT 12

Conservative

16;

Matches

ADR89339 standard; protein; 376 AA.

ADR89339

ADR89339
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New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 689; 122pp; English.
                                                                                                                                                                                                     Hinkle GJ, Slater SC,
                                                                                                            20-FEB-2003; 2003US-00369493
                                                                                                                              21-FEB-2002; 2002US-0360039P
                                                                                                                                                                                                                      WPI; 2004-061375/06.
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GOLDMAN B S.
                                                                                                                                                        HINKLE G J.
SLATER S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 376 AA;
                                                                         JS2003233675-A1.
                                                                                          18-DEC-2003.
                                                        Bacteria.
                                                                                                                                                         (HINK/)
(SLAT/)
(CHEN/)
                                                                                                                                                 CAOY/)
                                                                                                                                                                                    (COLD/)
                                                                                                                                                                                                     Cao Y,
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Goldman BS;

Chen X,

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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant comprising the recombinant DNA construct and growing the transformed plant with the recombinant DNA construct and growing the transformed plant, where the copylynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for improving plant with the improved plant properties, e.g. improved cold, heat or drought tolerance, colerance to herbicides, extreme osmocial conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modification of carbohydrate, introgen or content, improved yield by modification of carbohydrate, introgen or phosphorus use and/or uptake, by modification of photosynthesis or by production, improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition, improved plant growth and development of condition of production. This sequence represents a bacterial polypeptide used in the scome of the printed specification of photosynthesis or by formulation, more represents a bacterial polypeptide used in the form of the printed specification of production of production of the printed specification of particular of production of the printed specification of particular in electronic
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    100.0%; Score 86; DB 8; Length 376; 100.0%; Pred. No. 1.5e-06;
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                         Mismatches
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Query Match
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61 оккалуроўснальте 76

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ADN17733 standard; protein; 378 AA.
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RESULT 14
ADN17733
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Length 378; Indels

100.0%; Score 86; DB 8; I 100.0%; Pred. No. 1.5e-06; ive 0; Mismatches 0;

100.08;

Local Similarity 100. ses 16; Conservative

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Query Match

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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to promoter functional in a plant cell, where the promoter is positioned to promoter functional in a plant cell, where the promoter is positioned to promote for expression of a polynucleotide encoding a polyneptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant cannot be aving an improved property comprises transforming a plant with the cell combinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. Comprision to polynucleotide or polypeptide is useful for improving plants with the combinant DNA construct is useful for producing plants with construct set e.g. improved cold, heat or a drought colerance, increased rate of increased resistance to plant disease, better growth rate by modification of increased rate of the conformation, modified seed oil or protein yield and/or content, improved yield by modification of farbohydrate, introgen or phosphorus use and/or uptake, by modification of farbohydrate, nitrogen or content, improved plant growth and development under at least one stress condition, improved lighin production or improved galactomannan condition, improved lighin plant growth and development under at least one stress condition, improved lighin plant growth and development under at least one stress condition, improved lighin plant growth and development under at least one stress company in the production. Note: The sequence data for this patent did not company from part of the printed specification but was obtained in electronic command from part of the printed specification but was obtained in electronic command the production was obtained in electronic command the production or improved plant growth and electronic data for this patent did not command the plant growth and s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New recombinant DNA construct comprising a promoter positioned to provic
for expression of a polynucleotide encoding a polypeptide from a
microbial source, useful for producing plants with improved properties.
                                                                                                             Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell eycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
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                                                                  Bacterial polypeptide #386.
                      (first entry)
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SLATER S C.
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                      02-DEC-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HINK/)
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Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; of account tolerance; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide. ADS42875 standard; protein; 378 AA Hinkle GJ, Slater SC, Bacterial polypeptide #21305. 20-FEB-2003; 2003US-00369493. 21-FEB-2002; 2002US-0360039P (first entry) HINKLE G J. SLATER S C. GOLDMAN B S. US2003233675-A1. CHEN X. CAO Y. 02-DEC-2004 18-DEC-2003. ADS42875; Bacteria. (HINK/) (SLAT/) (CHEN/) (GOLD/) CAOY/) Cao Y, RESULT 15 ADS4287 

New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties. Goldman BS; Chen X, WPI; 2004-061375/06.

Claim 1; SEQ ID NO 21305; 122pp; English.

The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polymucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant such as maize or soybean. The method of producing a transformed plant with the such as maize or soybean. The method of producing a plant with the having an improved property comprises transformed plant, where the polymucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for improving plant properties. The recombinant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at segdata.uspto.gov/sequence.html.

Sequence 378 AA;

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                                Gaps
                                ô
   Length 378;
                               Indels
 100.0%; Score 86; DB 8; I
llarity 100.0%; Pred. No. 1.5e-06;
Conservative 0; Mismatches 0;
Query Match
Best Local Similarity
Matches 16; Conserv
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ò 셤 7, 2005, 07:40:32 Search completed: March Job time : 79.9868 secs

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7, 2005, 07:42:24 ; Search time 55.6291 Seconds (without alignments) 94.640 Million cell updates/sec
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1: \cgn2_6/ptodata/1/pubpaa/VSO7_PUBCOMB.pep:*

2: \cgn2_6/ptodata/1/pubpaa/RCT_MEW_PUB.pep:*

2: \cgn2_6/ptodata/1/pubpaa/NSO6_NEW_PUB.pep:*

4: \cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

5: \cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

6: \cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

7: \cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

8: \cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

9: \cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

11: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

12: \cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*

13: \cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*

14: \cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*

15: \cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*

16: \cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*

17: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*

18: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*

18: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*

19: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*

10: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1391452 seqs, 329044822 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                                                                                                                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                  Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 3, Appli	Sequence 1153, Ap	Sequence 1152, Ap	Sequence 689, App	Sequence 386, App	Sequence 21305, A	Sequence 10, Appl	Sequence 10, Appl	Sequence 27, Appl	Sequence 4, Appli	Sequence 4, Appli	444	Sequence 447, App
SUMMARIES	US-10-001-938-3	US-09-764-868-1153	US-09-764-868-1152	US-10-369-493-689	US-10-369-493-386	US-10-369-493-21305	US-09-756-983-10	US-09-828-574-10	US-10-001-938-27	US-10-299-540-4	US-10-299-184-4	US-10-239-313A-444	US-10-239-313A-447
DB	14	σ	ø	15	15	15	Q	0	14	14	14	14	14
% Query Match Length DB	16	340	341	376	378	378	15	15	. 15	15	15	15	16
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	94.2	94.2	94.2	94.2	94.2	94.2	94.2
Score	98	98	98	98	86	98	81	81	81	81	81	81	81
Result No.	1	7	٣	4	S	9	7	80	σ	10	11	12	13

RESULT 2 US-09-764-868-1153

Sequence 10648, A	Sequence 12087, A	Sequence 11, Appl	Sequence 5, Appli	Sequence 5, Appli	Sequence 8065, Ap	Sequence 21849, A	Sequence 22, Appl	Sequence 7330, Ap	Sequence 4573, Ap	Sequence 47, Appl	Sequence 13658, A	Sequence 8450, Ap		Sequence 15859, A	15487	9641,	18523	16754,	Seguence 19646, A	Sequence 9305, Ap	Sequence 634, App	Sequence 900, App	Seguence 6, Appli	Sequence 6, Appli	Seguence 12619, A	Sequence 10371, A	Seguence 23206, A		40315	Sequence 54551, A	Sequence 190831,	
US-10-369-493-10648	US-10-369-493-12087	US-09-828-574-11	US-10-299-540-5	US-10-299-184-5	US-10-369-493-8065	US-10-369-493-21849	US-10-375-010-22	US-10-369-493-7330	US-10-369-493-4573	US-10-369-493-47	US-10-369-493-13658	US-10-369-493-8450	US-09-861-451A-2	US-10-369-493-15859	US-10-369-493-15487	US-10-369-493-9641	US-10-369-493-18523	US-10-369-493-16754	US-10-369-493-19646	US-10-369-493-9305	US-10-474-776-634	US-10-472-928-900	US-10-299-540-6	US-10-299-184-6	US-10-369-493-12619	US-10-369-493-10371	US-10-369-493-23206	US-10-369-493-1212	US-10-767-701-40315	US-10-282-122A-54551	US-10-437-963-190831	
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365	376	15	15	15	382	384	376	379	380	376	374	378	368	375	376	358	379	385	369	362	378	378	15	15	423	360	372	376	175	297	362	
91.9	7.06	83.7	83.7	83.7	80.2	80.2	77.9	77.9	77.9	73.3	72.1	70.9	8.69	8.69	8.69	9.89	67.4	67.4	66.3	65.1	65.1	65.1	62.8	62.8	61.6	60.5	60.5	60.5	58.1	58.1	58.1	
79	78	72	72	72	69	69	67	67	67	63	62	61	60	9	9	59	28	28	57	26	26	26	54	54	23	52	25	52	20	20	20	
14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

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Sequence 3, Application US/10001938
; Sequence 3, Application US/10001938
; Sequence 3, Application US/20030031679A1
; SEQUENCE 4. INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: CARSON, Dennis
; APPLICANT: MARTINI, Alberto
; APPLICANT: MARTINI, Alberto
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES DERIVED FROM HEAT SHOCK PROTEINS AND US
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES DERIVED FROM HEAT SHOCK PROTEINS AND US
; TITLE OF INVENTION: UNMERS: US 60/245,181
; CURRENT APPLICATION NUMBER: US 60/245,181
; PRIOR FILING DATE: 2000-11-01
; CURRENT PILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PATENTIN OF SEQ ID NOS: 27
; SOFTWARE: PATENTIN OF SECOND 3:0
; FERROR OF SEQ ID NOS: 27
; SOFTWARE: PATENTING DATE: 2000-11-01
; FERROR OF SEQ ID NOS: 27
; SOFTWARE: PATENTING DATE: 2000-11-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-001-938-3
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, ORGANISM: Xenorhabdus nematophilus US-10-369-493-386
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Best Local Similarity 100.0%;
Matches 16; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 OKRAAYDQYGHAAFEQ 16
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT; ORGANISM: Escherichia coli
US-10-369-493-689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 16; Conservative
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US-10-369-493-386
                                JS-10-369-493-689
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                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: SITE
LOCATION: (110)
OTHER CONDITION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (216).
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-868-1153
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (135)

JTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Fatent No. US20020168711A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: NUCLEIC Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ32
CURRENT FPLING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper;
NUMBER OF SEQ ID NOS: 1510
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1152
LENGTH: 341
; Sequence 1153, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICATION:
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; SEQ ID NOS: 1510
; SEQ ID NO 1153
; EINGTH: 340
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Matches 16; Conservative
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; ORGANISM: Homo sapiens
US-09-764-868-1152
                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
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Best Local Similarity
Matches 16; Conserv
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US-09-764-868-1152
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LOCATION: (198
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Sequence 659, Application US/10354393
Sequence 650, Application US/1036518
Sequence Control Control Sequence Control C
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us-10-001-938-3.open.rapb

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JS-10-001-938-27
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ug-10-001-

APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/10/369,493
PRIOR FILLING DATE: 2003-02-28
PRIOR FILLING DATE: 2003-02-28
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 21305
LENGTH: 378
TYPE: PLANTER OF SEQ ID NOS: 47374
TYPE: PLANTER OF SEQ ID NOS: 47374
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Fatent No. US20020146759A1
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: ALBANI, Salvatore
TITLE OF INVENTION: SPREES PROTEINS AND PEPTIDES AND METHODS OF USE THEREOF
FILE REPERENCE: UCSD1310-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 378;
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APPLICANT: Albani, Salvatore

TITLE OF INVENTION: GHARACTERIZATION, QUANTIFICATION,
TITLE OF INVENTION: GHARACTERIZATION AND MODULATION OF
TITLE OF INVENTION: ANTIGEN-SPECIFIC T CELLS
FILE REFERENCE: 246/285-CIP
CURRENT APPLICATION NUMBER: US/09/756,983
CURRENT APPLICATION NUMBER: 60/105,018
PRIOR APPLICATION NUMBER: 60/105,018
PRIOR APPLICATION NUMBER: 60/105,018
PRIOR APPLICATION NUMBER: 99/421,506
PRIOR FILING DATE: 1999-10-19
PRIOR PRIOR DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 24

SOFTWARE: FREKSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 86; DB 15; 100.0%; Pred. No. 2.4e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: dnaJpl heat shock protein
US-09-756-983-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Xenorhabdus nematophilus
US-10-369-493-21305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OKRAAYDOYGHAAFEQ 16
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Best Local Similarity 100.0
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Best Local Similarity 100...
Local Similarity 100...
Local Similarity 100...
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ORGANISM: E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-756-983-10
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APPLICANT: THE RESENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: ALBANI, Salvatore
APPLICANT: CARSON, Dennis
APPLICANT: CARSON, Dennis
APPLICANT: PRAKKEN, Berent
APPLICANT: MARTINI, Alberto
TITLE OF INVENTION: THEREOF
FILE REPERENCE: UCSD1360-1
CURRENT APPLICATION NUMBER: US/10/001,938
CURRENT APPLICATION NUMBER: US 60/245,181
PRIOR APPLICATION DATE: 2000-11-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/10299540
Publication No. US20030143238A1
GENERAL INFORMATION.
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: THE RECENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: ALBAIL, Salvatore
TITLE OF INVENTION: ACAINST ARTHRITIOGENIC PEPTIDES INVOLVED IN THE PATHOGENESIS OF R
TITLE OF INVENTION: ACAINST ARTHRITIS
FILE REFERENCE: UCSD1370-7
CURRENT APPLICATION NUMBER: US/10/299,540
CURRENT APPLICATION NUMBER: US/10/299,540
FILE REPERIOR: US 09/616,247
PRIOR FILING DATE: 2000-07-14
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                                                                                                                                                                                                                                                                                                                                              Query Match 94.2%; Score 81; DB 9; L. Best Local Similarity 100.0%; Pred. No. 6.1e-07; Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
CURRENT APPLICATION NUMBER: US/09/828,574
CURRENT FILING DATE: 2001-04-06
PRIOR PLILING DATE: 2000-08-09
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 27, Application US/1001938 Publication No. US20030031679A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: dnaJP1 peptide US-09-828-574-10
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SOFTWARE: Patentin version 3.0
SEQ ID NO 27
LENGTH: 15
                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 OKRAAYDQYGHAAFE 15
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Best Local Similarity 100.0
Matches 15; Conservative
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ORGANISM: Escherichia coli
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Sequence 447, Application US/10239313A

Sequence 447, Application US/10239313A

Bublication No. US20030175285A1

GENERAL INFORMATION:
APPLICANT: KIINGUER - HAMOUR, Christine
APPLICANT: CORNAIA, Nathalie
APPLICANT: CORNAIA, Nathalie
APPLICANT: GORISCH, Liliane
TITLE OF INVENTION: NL-EEMINAL A GLUTAMINE IN THE FORM
TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
FRICH RAPLICATION NUMBER: PO0/03711
FRIOR FILLING DATE: 2002-09-19
FRIOR FILLING DATE: 2000-03-23
FRIOR PLICATION NUMBER: PCT 01/7072
FRIOR PLICATION NUMBER: 2010-03-22
FRIOR PLICATION NUMBER: PCT 01/7072
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        APPLICANT: GOETSCH, Liliane
APPLICANT: GOETSCH, Liliane
TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
FILE REFERENCE: 343 727 - US
CURRENT APPLICATION NUMBER: US/10/239,313A
CURRENT FILING DATE: 2002-09-19
PRIOR PRILING DATE: 2000-03-23
PRIOR PAPLICATION NUMBER: PCT 01/70772
PRIOR FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 697
SEQ ID NOS: 697
SEQ ID NO 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.2%; Score 81; DB 14; Length 15; 100.0%; Pred. No. 6.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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100.0%; Pred. No. 6.5e-07;
tive 0; Mismatches 0;
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Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.2.
100.0%; F1.
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Matches 15; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 15; Conserv
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US-10-369-493-10648
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US-10-239-313A-447
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| Sequence 4, Application US/10299184
| Publication No. US2030147910A1
| Publication No. US2030147910A1
| Publication No. US2030147910A1
| APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
| APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
| APPLICANT: ALBANI, Salvatore
| TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN INDUCING IMMUNE PROTEC
| TITLE OF INVENTION: ARTHRITIS
| FILE REFERENCE: UCSD1370-6
| CURRENT APPLICATION NUMBER: US 09/616,247
| PRIOR PELING DATE: 1998-06-30
| PRIOR PELING DATE: 1998-06-30
| PRIOR PELING DATE: 1998-06-30
| PRIOR PELING DATE: 1994-05-20
| WUMBER OF SEQ ID NOS: 10
| SOFTWARE: PATEURIN VERSION 3.1
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PRIOR APPLICATION NUMBER: US 09/107,615
PRIOR FILING DATE: 1998-06-30
PRIOR PILING DATE: 1998-06-30
PRIOR PILING DATE: 1998-03-15
PRIOR PILING DATE: 1994-05-20
PRIOR PILING DATE: 1994-05-20
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 4
SEQ ID NO 4
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Publication No. US20030175285A1
GENERAL INFORMATION:
APPLICANT: KLINGUER - HAMOUR, Christine
APPLICANT: CORVAIA, Nathalie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Synthetic dnaJpl
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US-10-299-540-4
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ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial sequence
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Matches 15; Conservative
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Best Local Similarity
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Sequence 12087, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Gao, Yongwei

APPLICANT: Slater, Steven C.

APPLICANT: Slater, Steven C.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10 (52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT PILING DATE: 2003-02-28

PRIOR FILING DATE: 2003-02-21

NUMBER OF SEQ ID NOS: 47374

LENGTH: 376

TYPE: PRI
                APPLICANT: Chen, Xianteng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 10648
LENGTH: 365
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90.7%; Score 78; DB 15; Length 376;
Best Local Similarity 87.5%; Pred. No. 5.5e-05;
Matches 14; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Sphingomonas aromaticivorans
US-10-369-493-10648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 QKRAAYDRFGHAAFEQ 75
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US-10-369-493-12087
Goldman, Barry S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
US-10-369-493-12087
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Search completed: March 7, 2005, 08:45:18 Job time: 55.6291 secs

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Sequence 5912, Ap
Sequence 2, Appli
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Sequence 4, Appli
Sequence 10, Appli
Sequence 5, Appli
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Sequence 2, Appli
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Sequence 6, Appli
Sequence 4647, Ap
Sequence 6, Appli
Sequence 17703, Ap
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Sequence 1869, Ap
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                                                                          March 7, 2005, 07:23:03; Search time 19.8146 Seconds (without alignments) 60.278 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                          Issued Patents AA:*

1. /cgn2_6/ptodate/1/iaa/5A_COMB.pep:*

2. /cgn2_6/ptodate/1/iaa/6B_COMB.pep:*

3. /cgn2_6/ptodate/1/iaa/6A_COMB.pep:*

4. /cgn2_6/ptodate/1/iaa/6B_COMB.pep:*

5. /cgn2_6/ptodate/1/iaa/6B_COMB.pep:*

6. /cgn2_6/ptodate/1/iaa/FB_COMB.pep:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-618-869-4
US-09-518-869-4
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US-09-518-869-2
US-09-618-869-2
US-09-618-869-2
US-09-618-869-2
US-09-107-615-4
US-08-107-615-4
US-08-107-615-5
PCT-US95-0486-5
US-09-107-615-5
PCT-US95-0486-5
US-09-107-615-5
US-09-56-991A-27174
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US-09-581-10-4647
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US-09-581-10-4647
US-09-107-413-3487
US-09-107-615-6
US-09-107-615-8
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Maximum Match 100%
Listing first 45 summaries
                                                      protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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Perfect score:
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Sequence 11, Appl
Sequence 17628, A
Sequence 10, Appl
Sequence 29, Appli
Sequence 30, Appli
Sequence 28, Appli
Sequence 28, Appli
Sequence 24, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 6832, A
Sequence 6832, A
Sequence 11497, A
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      US-09-908-992B-11
US-09-248-796A-17628
US-09-908-992B-10
US-09-908-992B-9
US-09-908-992B-9
US-09-908-992B-9
US-09-908-992B-8
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US-09-908-992B-8
US-09-908-992B-4
US-09-998B-44-4
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US-09-949-016-6832
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naturally folded and secreted prote
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; TYPE: PRT
; ORGANISM: E. coli
US-09-553-498-4
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1 OKRAAYDQYGHAAFEQ 16 84 QKRAAYDQYGHAAFEQ

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APPLICANT: Ambrosius, Dorthee
APPLICANT: Rudolph, Rainer
APPLICANT: Rudolph, Rainer
APPLICANT: Schaeffner, Joed
APPLICANTION: SECRETED PROTEINS BY CO-SECRETION OF MOLECULAR
TITLE OF INVENTION: CHAPERONES
FILE REFERENCE: 20381
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: EP99114811.5
PRIOR APPLICATION NUMBER: EP99114811.5
NUMBER OF SEC ID NOS: 10
SOFTWARE: Patentin Ver. 2.1 Sequence 4, Application US/09618869; Patent No. 6455279; GENERAL INFORMATION:

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APPLICANT: Ambrosius, Dorothee
APPLICANT: Rudolph, Rainer
APPLICANT: Schaeffner, Joerg
TITLE OF INVENTION: Process for the production of naturally folded and secreted protes;
FILE REFERENCE: Case 20379
CURRENT APPLICATION NUMBER: 108/09/553,498
CURRENT FILING DATE: 1999-04-26
RIOR APPLICATION NUMBER: EP99107412.1
PRIOR FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 2
LENGTH: 399
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APPLICANT: Rudolph, Rainer
APPLICANT: Schwarz, Josep
APPLICANT: Schwarz, Elisabeth
TITLE OF INVENTION: PROCESS FOR THE PRODUCTION OF NATURALLY FOLDED AND
TITLE OF INVENTION: SECRETED PROTEINS BY CO-SECRETION OF MOLECULAR
TITLE OF INVENTION: CHAPERONES
FILLE REFERENCE: 20381
CURRENT APPLICATION NUMBER: US/09/618,869
FRIOR APPLICATION NUMBER: EP99114811.5
PRIOR APPLICATION NUMBER: EP99114811.5
PRIOR FILING DATE: 1999-07-29
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; Patent No. 5773570
; GENERAL INFORMATION:
; APPLICANT: CASSON, DENNIS A.
; APPLICANT: ALBANI, SALVATORE
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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100.0%; Score 86; DB 4; 1
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 16; Conservative 0; Mismatches 0;
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Patent No. 6455279
GENERAL INFORMATION:
                                             Sequence 2, Application US/09553498 Patent No. 6309861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%;
Matches 16; Conservative 0;
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US-09-618-869-2
                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: E. coli
US-09-553-498-2
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SEQ ID NO 2
LENGTH: 399
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Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY RRETON:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION:
TITLE OF INVENTION: US/09/543,681A
CURRENT PELLOTATION NUMBER: US/09/543,681A
CURRENT PELLOGATION NUMBER: US 60/128,706
PRIOR PELLOTATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 5912
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Patent No. 6610836
GENERAL INFORMATION
FOR ATTORNATION
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
CURRENT FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 9011
LENGTH: 380
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100.0%; Score 86; DB 4; Length 380;
Best Local Similarity 100:0%; Pred. No. 3.4e-07;
Matches 16; Conservative 0; Mismatches 0: Indels
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                                                                                                                                        100.0%; Score 86; DB 4; Length 131; 100.0%; Pred. No. 1.1e-07; ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 3.4e-07;
tive 0; Mismatches 0;
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; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9011
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                                                                                                                                                                                                                                                                                          84 OKRAAYDOYGHAAFEO 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Proteus mirabilis
                                ; TYPE: PRT;
; ORGANISM: Escherichia coli
US-09-618-869-4
                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 16; Conservative
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US-09-543-681A-5912
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                      LENGTH: 131
SEQ ID NO 4
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Gaps
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APPLICANT: ALDani, Salvatore
TITLE OF INVENTION: METHODS FOR ISOLATION, QUANTIFICATION,
TITLE OF INVENTION: AMTIGEN-SPECIFIC T CELLS
TITLE REPERRNCE: 246/288-CIP
CURRENT PAPLICATION NUMBER: US/09/756,983
CURRENT FILING DATE: 2001-01-09
PRIOR FILING DATE: 1998-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FRAETSEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 10
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 15;
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      PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3; Le
. 8.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.2%; Score 81; DB 4; Le
100.0%; Pred. No. 8.2e-08;
tive 0; Mismatches 0;
                                                                                        FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/618,464
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: HOWELLS, STRAY L.
REGISTRATION NUMBER: 34,842
RESTERENCE/DOCKET VUMBER: 07340/042001
TELEPRANCE/DOCKET VUMBER: 07340/042001
TELEPRANCE/DOCKET VUMBER: 07340/042001
TELEPRANCE/DOCKET VUMBER: 07340/042001
TELEPRANCE/DOCKET NUMBER: 07340/042001
TELEPRANCE/DOCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , OTHER INFORMATION: dnaJpl heat shock protein
US-09-756-983-10
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Pred. No.
                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,615
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: Immunogenic dnaJ Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/09756983
Patent No. 6787154
GENERAL INFORMATION:
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Best Local Similarity 100.0%; P.
Matches 15; Conservative 0;
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY:
; LOCATION:
US-09-107-615-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-756-983-10
      SOFTWARE:
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   IMMUNE PROTECTION AGAINST ARTHRITC
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ARTHRITOGENIC PEPTIDES INVOLVED IN
THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
   INDUCING IMMUNE PROTEC
INVOLVED IN
THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.2%; Score 81; DB 1; Length 15; 100.0%; Pred. No. 8.2e-08;
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                                                                                                                                                                                                                                                                   COUNTY: US
ZIP: 92037
ZIP: 92037
ZIP: P2037
ZIP: P2037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,464
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ADDRESSEE: FISH & RICHARDSON P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                 ADDRESSEE: FISH & RICHARDSON P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Prec. ... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INPORMATION:
NAME: HOWELLS, STACY L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/042001
TELECOMMUNICATION INFORMATION:
TELEFAX: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: Immunogenic dnaJ Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
US-09-107-615-4
Sequence 4, Application US/09107615
Patent No. 6153200
GENERAL INFORMATION:
GENERAL GRESON, DENNIS A.
APPLICANT: ALBANI, SALVATORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 OKRAAYDQYGHAAFE 15
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Best Local Similarity 100.0
Matches 15, Conservative
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TITLE OF INVENTION: INDC
TITLE OF INVENTION: INVC
TITLE OF INVENTION: THE
NUMBER OF SECUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
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TITLE OF INVENTION: IN
TITLE OF INVENTION: AT
TITLE OF INVENTION: TH
NUMBER OF SEQUENCES: 6
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CLASSIFICATION: 424
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: US
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; LOCATION: 1..15
US-08-618-464-4
                                                                                                                                                                                                                CITY: La Jolla
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid STRANDEDNESS: 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: La Jolla
STATE: CALIFORI
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Gaps
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ARTHRITOGENIC PEPTIDES INVOLVED IN
THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTLE OF INVENTION: ABLVATIONS AND METHODE TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODE TITLE OF INVENTION: NATHRITOGENIC PEPTIDES INVOLVED TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ? NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS: ADDRESSES: FISH & RICHARDSON P.C. STREET: 4225 Executive Square, Suite 1400 CITY: La Jolla & RICHARDSON P.C. STREET: 4225 Executive Square, Suite 1400 CITY: La Jolla & COUNTRY: US STATE: CALIFORNIA COUNTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN DATA: APPLICATION NUMBER: US/09/107,615
                                                                                                                                                        CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/618,464

FILING DATE:

CLASSIFICATION: 424

ATTOREY/AGENT INFORMATION:

NAME: HOWELLS, STACK I.

REGISTRATION NUMBER: 34,842

REGISTRATION NUMBER: 34,842

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF SECUED NO: 5:

SEQUENCE CHRARACTERISTICS:

LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 72; DB 1;
Pred. No. 3.1e-06;
1; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: Immunogenic dnaJ Peptide
                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/09107615
Patent No. 6153200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.7%;
92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 KRAAYDQYGHAAFE 15
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US.
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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APPLICANT: CARSON,
APPLICANT: ALBANI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
TOPOLOGY: lir
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US-08-618-464-5
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APPLICANT: CARSON, DENNIS A.

APPLICANT: ALBANI, SALVATORE
TITLE OF INVENTION: UACCINE COMPOSITIONS AND METHODS USEFUL IN
TITLE OF INVENTION: INDUCING
TITLE OF INVENTION: INVOLVED IN
TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                             Sequence 4, Application PC/TUS9504896
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY
APPLICANT: OF CALIFORNIA
TITLE OF INVENTION: METHOD AND REAGENTS FOR THE TREATMENT
TITLE OF INVENTION: OF RHEUMATOID ARTHRITIS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBBINS, BERLINER & CARSON
STREET: 201 N. FIGUEROA STREET, 5TH FLOOR
CITY: LOS ANGELS
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.2%; Score 81; DB 5; Length 15; 100.0%; Pred. No. 8.2e-08;
                                                                                                                                                                                                                                                                                                                                                                            COUNTER TOTAL COUNTER TO THE TOTAL COUNTER TOTAL COMPUTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: PCT/US95/04896
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4225 Executive Square, Suite 1400
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:ive 0; Mismatches
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IMMEDIATE SOURCE:
CLONE: Immunogenic dnaJ Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: BERLINER, ROBERT
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555-
TELECOMUNICATION INFORMATION:
TELEPHONE: 213-977-1001
TELEPHONE: 213-977-1003
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08618464 Patent No. 5773570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 15; Conservative
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STREET: 42:
                                            RESULT 10
PCT-US95-04896-4
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US-08-618-464-5
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; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2899
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Job time: 20.8146 secs
       1..15
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     ; LOCATION:
PCT-US95-04896-5
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APPLICANT: THE REGENTS OF THE UNIVERSITY
APPLICANT: THE REGENTS OF THE UNIVERSITY
TITLE OF INVENTION: METHOD AND REAGENTS FOR THE TREATMENT
ITILE OF INVENTION: OF RHEUMATOID ARTHRITIS
TITLE OF INVENTION: OF RHEUMATOID ARTHRITIS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBBINS, BERLINER & CARSON
STREET: 201 N. FIGUEROA STREET, 5TH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                         Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATR:
APPLICATION NUMBER: PCT/US95/04896
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         Score 72;
                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No
                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: Immunogenic dnaJ Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: Immunogenic dnaJ Peptide
ATTORNEY/AGENT INFORMATION:
NAME: HOWELLS, STACY L.
REGISTRATION NUMBER: 34,842
REFRENCE/DOCKET NUMBER: 0734(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: BERLINER, ROBERT
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213-977-1001
                                                                                                                                                                                                                                                                                                                                                                                                         83.7%;
92.9%;
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . TELEFAX: 213-977-1003
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                              Peptide
1..15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: Peptide
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CLASSIFICATION:
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COUNTRY: US
ZIP: 90012
                                                                                                                                                                                                                                                                                                                          NAME/KEY:

COCATION:

US-09-107-615-5
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Sequence 2899, Application US/09540236

Sequence 2899, Application US/09540236

Patent No. 6673910

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR.
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
SEQ ID NOS: 3840

LENGTH: 407
                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AREUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27174
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                                              Gaps
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Pred. No. 0.0056;
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Pred. No. 0.009;
4; Mismatches 2; Indels
Score 72; DB 5; Length 15;
Pred. No. 3.1e-06;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                             Sequence 27174, Application US/09252991A Patent No. 6551795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.1%;
78.6%;
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62.5%;
Query Match
Best Local Similarity 92.9%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KRAAYDQYGHAAFE 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 KRAAYDQYGHAGVD 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 OKRAAYDOYGHAAFEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 72.13
Best Local Similarity 78.6
Matches 11; Conservative
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Best Local Similarity 62.5
Matches 10, Conservative
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I'ilis Fage Blank (usptc)

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

7, 2005, 09:43:27; Search time 38 Seconds (without alignments) 40.512 Million cell updates/sec March Run on:

US-10-001-938-3 Perfect score:

1 OKRAAYDQYGHAAFEQ 16 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues

2773 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 16

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	perisulfakinin - A	neosulfakinin-II -	leucosulfakinin-II		T-cell antigen rec	-cell		_					antigen z	ptor	hemoglobin beta ch	T-cell receptor be	lymnaDFamide 1 - g	-D-J	Ig H chain V-D-J r	Ig H chain V-D-J r	glucose-6-phosphat	lymnaDFamide 2 - g	factor X activator	T-cell antigen rec	lymnaDFamide 3 - g	Ig heavy chain DJ	T-cell receptor be	-cel	T-cell receptor be
OUTTER	A60656	A56632	GMROL2	B60656	S47372	S47384	GMROL	S47368	S47359	847365	S47374	PT0214	S47388	PH1479	152618	PH0770	S32471	PH1586	PH1622	PH1589	S11078	S32472	A60379	S47383	S32473	PH1319	F28587	I53284	PT0215
DB	7		-			•		7	•	•	•	7	•	7	4		•	0	0							(1			
% Query Match Length	11	14	10	10	13	13	11	13	13	13	13	11	13	13	14	15	13	14	16	16	80	13	13	13	13	15	15	15	10
% Query Match	39.5	39.5	9	36.0	36.0	36.0	34.9	34.9	32.6	ς.	ď	30.2	30.2	30.2	30.5	30.5	29.1	29.1	27.9	27.9	26.7	26.7	26.7	25.6	25.6	25.6	25.6	25.6	24.4
Score	34	34	31	31	31	31	30	30	28		28	26	26	26	26	56	25	25	24	24	23	23	23	22	22	22	22	22	21
Result No.	-	8	ო	4	.C	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

T-cell receptor be	T-cell receptor be	T-cell receptor be	T-cell antigen rec	collecting duct wa	lymnaDFamide 4 - g	photosystem II oxy	T-cell receptor be	glucose 1-dehydrog	extension protein	unidentified QR310	Ig heavy chain CRD	R-phycoerythrin ga	phosphopyruvate hy	photosystem II oxy	Ig heavy chain CRD
PH0746	PH0771	PH1461	S47361	151905	S32474	G44957	PH0755	A17150	S48685	PC4269	PT0309	G22565	PN0168	PA0013	PT0232
N	~	~	N	~	~	N	~	~	~	~	N	N	N	~	0
12	. 12	12	13	13	13	14	14	14	14	15	10	13	13	14	14
24.4	24.4	24.4	24.4	24.4	24.4	24.4	24.4	24.4	24.4	24.4	23.3	23.3	23.3	23.3	23.3
21	21	21	21	21	21	21	21	21	21	21	20	50	20	20	20

RESULT 1

.

perisulfakinin - American cockroach

C;Species: Periplaneta americana (American cockroach)
C;Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 09-Jul-2004
C;Accession: A60656
R;Veenstra, J.A.
Neuropeptides 14, 145-149, 1989
A;Title: Isolation and structure of two gastrin/CCK-like neuropeptides from the American A;Reference number: A60656; MUID:90137190; PMID:2615921

A;Accession: A60656 A;Molecule type: protein A;Residues: 1-11 <VEE>

A,Cross-references: UNIPROT:P36885 C;Comment: This neuropeptide stimulates hindgut contractions. C;Kowords: amidated carboxyl end; neuropeptide; sulfoprotein F;G/Binding site: sulface (Tyr) (covalent) #status experimental F;11/Modified site: amidated carboxyl end (Phe) #status experimental

Gaps ö Query Match 39.5%; Score 34; DB 2; Length 11; Best Local Similarity 55.6%; Pred. No. 8.8; Matches 5; Conservative 1; Mismatches 3; Indels

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6 YDQYGHAAF 14 FDDYGHMRF 11 ઠે 셤

neosulfakinin-II - flesh fly (Sarcophaga bullata)

NiAlternate names: Neb-SK-II
NiContains: neosulfakinin-I (Neb-SK-I)
NiContains: neosulfakinin-I (Neb-SK-I)
NiContains: neosulfakinin-I (Neb-SK-I)
Cipecies: Sarcophaga bullata
Cipaces: 21-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004
Cipaces: 1-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004
Cipacession: As6632
Comp. Biochem. Physiol. C 103, 135-142, 1992
A;Title: Isolation and primary structure of two sulfakinin-like peptides from the fleshf A;Reference number: A56632; MUID:93083101; PMID:1360367

A, Accession: A5632
A, Molecule type: protein
A, Residues: 1-14 < FFON>
A, Cross-references: UNIPROT: P41493
A, Experimental source: heads

A.Note: sequence extracted from NCBI backbone (NCBIP:120391)
C,Keywords: amidated carboxyl end, neuropeptide; sulfoprotein
F;1-14/Product: neosulfakinin-II #status experimental «NSK2»
F;6-14/Product: neosulfakinin-I #status experimental «NSK1»
F;9/Binding site: sulfate (Tyr) (covalent) #status predicted
F;9/Binding site: amidated carboxyl end (Phe) #status experimental

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Richner, P.J. submitted to the EMBL Data Library, August 1994 submitted to the EMBL Data Library, August 1994 A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T ct A;Reference number: 847355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: A01622
R;Nachman, R.J.; Holman, G.M.; Haddon, W.F.; Ling, N.
R;Nachman, R.J.; Holman, G.M.; Haddon, W.F.; Ling, N.
R;Science 1.T.13, 198
A;Title: Leucosulfakinin, a sulfated insect neuropeptide with homology to gastrin and cht A;Reference number: A01622; MUD:86315858; PMID:3749893
A;Accession: A01622
A;Accession: A01622
A;Accession: A01622
A;Reference number: A01622
A;Reference numbe
                             submitted to the EMBL Data Library, August 1994
A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T ct
A;Reference number: S47355
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
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C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-13 - LEBH-
A;Cross-references: EMBL:Z35704; NID:g527501; PIDN:CAA84773.1; PID:g527502
C;Keywords: T-cell receptor
                                                                                                                                                                      A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 -4.EH>
A;Cross-references: EMBL:Z35697; NID:g527485; PIDN:CAA84766.1; PID:g527486
C;Keywords: T-cell receptor
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C;Kaywords: amidated carboxyl end; hormone; sulfoprotein
F;6/Binding site: sulfate (Tyr) (covalent) #status experimental
F;11/Modified site: amidated carboxyl end (Phe) #status experimental
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Pred. No. 35;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                     Score 31; DB
Pred. No. 35;
2; Mismatches
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71.4%;
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Best Local Similarity 71.4%;
Matches 5; Conservative
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3 FEDYGHMRF 11
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                        A; Accession: S47372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: A26335
R;Nachman, R.J.; Holman, G.M.; Cook, B.J.; Haddon, W.F.; Ling, N.
Biochem. Biophys. Res. Commun. 140, 357-364, 1986
A;Title: Leucosulfakinin-II, a blocked sulfated insect neuropeptide with homology to chc A;Reference number: A26335; MUID:87048769; PMID:3778455
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Neuropeptides 14, 145-149, 1989

Affile: Isolation and structure of two gastrin/CCK-like neuropeptides from the American A; Reference number: A60656; MUID:90137190; PMID:2615921

A; Recession: B60656

A; Moceule type: protein

A; Residues: 1-10 <VEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:P09039
C;Comment: This peptide was isolated from head extracts. It stimulates muscle contractio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: gastrin
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid; sulfoprotein
C;Keywords: amidated carboxyl end; caid (Gln) #status experimental
F;5/Binding site: sulfate (Tyr) (covalent) #status experimental
F;10/Modified site: amidated carboxyl end (Phe) #status experimental
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T-cell antigen receptor VJ junction beta chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Periplaneta americana (American cockroach)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C;Accession: B60656
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Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 31; DB 1; Length 10;
Pred. No. 27;
0; Mismatches 3; Indels
                                                                         3; Indels
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Score 34; DB 2
Pred. No. 11;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                leucosulfakinin-II - Madeira cockroach
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   39.5%;
   Query Match 39.5
Best Local Similarity 55.6
Matches 5; Conservative
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Best Local Similarity
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Best Local Similarity
Matches 5; Conserva
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RiLehner, P.J.
submitted to the EMBL Data Library, August 1994
A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c
A;Reference number; 847355
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C,Accession: PT0214
C,Accession: PT0214
S,Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
J. Exp. Mac. 173, 1091-1097, 1991
A,Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restric A,Reference number: PT0209; MUID:91217621; PMID:1902501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Cross-references: EMBL:Z35699; NID:g527491; PIDN:CAA84768.1; PID:g527492; EMBL:Z35689; ;Accession: S47399; ;Status: preliminary
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C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence revision 25-Oct-1996 #text_change 05-Nov-1999
C:Accession: 847374; 847399; 847364
                                                                                                                               A;Cross-references: EMBL:Z35708; NID:g527509; PIDN:CAA84777.1; PID:g527510 A;Accession: S47396
                                                                                                                                                                                                                                                                              ;Cross-references: EMBL:Z35674; NID:g527527; PIDN:CAA84743.1; PID:g527528; Accession: S47397
;Accession: S47397
;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-13 <LE5>
A;Cross-references: EMBL:235675; NID:g527529; PIDN:CAA84744.1; PID:g527530
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A;Status: preliminary
A;Molecule +ype: manA
A;Residues: 1-13 <LE6>
A;Cross-references: EMBL:Z35676; NID:g527531; PIDN:CAA84745.1; PID:g527532
C;Keywords: T-cell receptor
A;Cross-references: EMBL:Z35700; NID:g527493; PIDN:CAA84769.1; PID:g527494
A;Accession: S47379
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A;Residues 1.13 - LLE2>
A;Cross-references: EMBL:Z35677; NID:G527533; PIDN:CAA84746.1; PID:G527534
C;Keywords: T-cell receptor
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T-cell receptor beta chain V-J region (4-1-L.6) - mouse (fragment)
C;Species: Mus musculus (house mouse)
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Pred. No. 1.2e+02;
3; Mismatches 0; Indels
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Best Local Similarity 57.1%;
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserva
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6 RSSYEQY 12
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                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <LE4>
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                                                                                      A, Molecule type: mRNA
A, Residues: 1-13 <LE3>
                                                           Status: preliminary
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A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Coss-references: EMBL:Z35690; NID:g527471; PIDN:CAA84759.1; PID:g527472; EMBL:Z35679;
A;Accession: S47375
A;Accession: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <LE2>
                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47368
R;Lehner, P.J.
Submitted to the EMBL Data Library, August 1994
A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T A;Accession: S47358
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47365; S47375; S47379; S47397; S47398; S47355
R;Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by TA:Reference number: S47355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: Oc-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: 847359
R;Lehner, P.J.
R;Lehner, P.J.
A;Description: Human HiA-A0201 restricted recognition of influenza A is dominated by TA.Reference number: 847355
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A;Status: preliminary
A;Molecule type: mkNA
A;Residues: 1-13 <LENA
A;Reserences: EMBL:Z35683; NID:g527455; PIDN:CAA84752.1; PID:g527456
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:235693; NID:g527477; PIDN:CAA84762.1; PID:g527478
C;Keywords: T-cell receptor
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S47365
T-cell antigen receptor VJ junction beta chain - human
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57.1%;
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Best Local Similarity 57.1
Matches 4; Conservative
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RGAYEQY 12
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RSSYEQY 12
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A;Molecule type: mRNA
A;Residues: 1-13 <LEH>
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A.Title: Dominant beta-thalassaemia trait in a Portuguese family is caused by a deletion A.Reference number: 152618; MUID:92068764; PMID:1659862
                                                                                                           A;Molecule type: DNA
A;Residues: 1-14 <ONE>
A;Cross-references: GB:S68042; NID:g239717; PIDN:AAB20440.1; PID:g239718
                                                                                                                                                                                                                                                                                                        Score 26; DB 4; Length 14; Pred. No. 2.9e+02; Mismatches 3; Indels
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A, Map position: 11p15.4-11p15.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: March 7, 2005, 09:58:38
                                                             A;Accession: 152618
A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                        Query Match 30.2%;
Best Local Similarity 50.0%;
Matches 5; Conservative
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J. Exp. Med. 177, 811-820, 1993
A;Title: T cell receptor selection by and recognition of two class I major histocompatib A;Reference number: PH1430; MUID:93171821; PMID:8436911
A;Accession: PH1479
                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47388
R;Lehner, P.J.
submitted to the EMBL Data Library, August 1894
A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T.A.Reference number: S47355
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C;Species: Homo sapiens (man)
C;Date: 02-ul-1996 #sequence_revision 11-Jul-1996 #text_change 20-Apr-2000
C;Accession: 152618
R;Oner, R.; Oner, C.; Wilson, J.B.; Tamagnini, G.P.; Ribeiro, L.M.; Huisman, T.H. Br. J. Haematol. 79, 306-310, 1991
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C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 15-Mar-2004
C;Accession: PH1479
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A;Molecule type: mRNA
A;Residues: 1-13 <LEH>
A;Cross-references: EMBi:Z35710; NID:g527515; PIDN:CAA84779.1; PID:g527516
C;Keywords: T-cell receptor
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                                                                                                                               Score 26; DB 2; Length 11;
Pred. No. 2.2e+02;
1; Mismatches 2; Indels
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Pred. No. 2.6e+02;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                      RESULT 13
847388
T-cell antigen receptor VJ junction beta chain - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-13 <CAS>
A;Experimental source: cytolytic T-lymphocyte
C;Keywords: receptor; T-cell
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71.4%;
                                                                                                                                  30.2%;
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                              A,Molecule type: mRNA
A,Residues: 1-11 <NAK>
C,Keywords: T-cell receptor
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RGTYEQY 10
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RAAVEQY 12
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5 QAGYEQY 11
                                                                                                                               Query Match
Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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          A; Accession: PT0214
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OM protein - protein search, using sw model

March 7, 2005, 09:10:02; Search time 172 Seconds (without alignments) 47.635 Million cell updates/sec Run on:

US-10-001-938-3 86 Title: Perfect score:

1 OKRAAYDQYGHAAFEQ 16 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1612378 seqs, 512079187 residues Searched:

Total number of hits satisfying chosen parameters:

7514

Minimum DB seq length: 0 Maximum DB seq length: 16

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	P41492 sarcophaga	P36885 periplaneta	P41493 sarcophaga	P47733 locusta mig		P67803 periplaneta	P04428 leucophaea	P80178 lymnaea sta	Q7s2j9 neurospora	082402 fragaria nu		082405 fragaria ii	O82406 fragaria mo				Q71z24 vipera aspi			_		Q6urv3 sorghum bic	O9tnp2 homo sapien	Q98898 lycopersico			Q80y03 rattus sp.				Q93le4 heliobacill
SUMMAKIES		σī	NSK1_SARBU	LSKP_PERAM	NSK2 SARBU	LOSK_LOCMI	LSK2_LEUMA	LSK2_PERAM	LSK1_LEUMA	NP1_LYMST	Q7S2J9	082402	082404	082405	082406	082407	082781	NP2_LYMST	Q71. <u>Z</u> 24	Q9S8A0	Q71UL3	Q68D59	NP3_LYMST	Q6URV3	Q9TNP2	095898	NP4_LYMST	PSBP PINPS	Q80Y03	Q7M0K1	ECDA_LYMDI	Q9TRR1	Q93LE4
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RESULT 2

D. Liskp Peram STANDARD; PRT; 11 AA.
P368B5.
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T 01-JUN-1994 (Rel. 29, Last sequence update)
T 01-JUN-1994 (Rel. 44, Last annotation update)
E Perisulfakinin (Pea-Sk-1).
S Perisulfakinin (Pea-Sk-1).
C Bukaryota; Merazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
C Neoptera; Orthopteroidea; Dictyoptera; Blattoidea;
C Blattidae; Periplaneta.
X NCBI\_TaxID=6978;
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		PRT; 9 AA. ed) sequence update) annotation update)	(Neobe apoda; rachyce	van Damme of two sulf 1.";	creted. he gastrin/cholecystoki quencing; Neuropeptide; Sulfotyrosine (Potenti Phenylalanine amide (P	re 34; DB d. No. 1.6 Mismatches
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Schoofs L., Holman G.L., Hayes T.K., Nachman R.J., de Loof A.;

(In) McCaffery A., Wilson I. (eds.);

(In) PROSIDE Belongs to the gastrin/cholecystokinin family.

(In) McCaffery Belongs to the gastrin/cholecystokinin family.

(In) McCaffer Belongs to the gastrin family.

(In) McCaffer Belongs 
05-JUL-2004 (Rel. 44, Last annotation update)
Sulfakinin (LOM-SK).
Locusta migratoria (Wigratory locust).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Oedipodinae; Locusta.
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Pred. No. 1e+02;
0; Mismatches 4; Indels
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60.0%;
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62.5%;
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10 AA; 1255 MW;
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                                                                                                                                                                                                                                                                                                TISSUE=Brain;
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LSK2 LEUMA
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Neosulfakinin-11 (Nels-Sk-11)
Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
Sukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota;
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Oestroidea;
Sarcophagidae, Sarcophaga.
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"Isolation and primary structure of two sulfakinin-like peptides from
the fleshfly, Neobellieria bullata.";
Comp. Biochem. Physiol. 103C:135-142(1992).
-!-FONCTION: Myctropic peptide.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBLIARITY: Belongs to the gastrin/cholecystokinin family.
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                                                                                        Membrason.

Weenstra J.A.;

"Isolation and structure of two gastrin/CCK-like neuropeptides from the American cockrach homologous to the leucosulfakinins.";

Neuropetides 14:145-149(1989).

-!- FUNCTION: Stimulates hindgut contractions.

-!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.

PIN: A60655, A60655.

InterPro; IPRO01651; Gastrin.

PROSITE; PS00259; GASTRIN; 1.

Amidation; Direct protein sequencing; Hormone; Sulfation.

MOD RES

6 Sulfotyrosine.
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                                            TISSUE=Corpora cardiaca;
MEDLINE=90137190; PubMed=2615921; DOI=10.1016/0143-4179(89)90038-3;
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InterPro; IPR001651; Gastrin.
PROSITE; PS00259; GASTRIN; 1.
Amidation; Direct protein sequencing; Neuropeptide; Sulfation.
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Phenylalanine amide (Potential)
8B4E06D5B61C62AA CRC64;
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Pred. No. 61;
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8B4E0680E86B5AAA CRC64;
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(Rel. 33, Last sequence update)
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Nachman R.J., Holman G.M., Cook B.J., Haddon W.F., Ling N.;
Nachman R.J., Holman G.M., Cook B.J., Haddon W.F., Ling N.;
"Leucosulfakinin-II, a blocked sulfated insect neuropeptide with
homology to cholecystokinin and gastrin.";
Blochem. Biophys. Res. Commun. 140:357-364(1986).
-!-FUNCTION: Changes the frequency and amplitude of contractions of
the cockroach hingut. Stimulates muscle contraction of hindgut.
-!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
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PIR; A26315; GMROLZ.

InterPro; IPRO01651; Gastrin.

PROSITE; PS00259; GASTRIN; 1.

Amidation; Direct protein sequencing; Hormone;

Amidation or protein sequencing; Hormone;

Pyrrolidone carboxylic acid.

Pyrrolidone carboxylic acid.

Pyrrolidone carboxylic acid.
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Pred. No. 1.8e+02;
0; Mismatches 3; Indels
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9B4F5391E86B5AAA CRC64;
10 AA.
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LSK2 PERAM

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SEQUENCE

LISK2 PERAM

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TO 1-R003,

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Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D., Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M., Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M., Selitremikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D., Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S., Kamal M., Kamwysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
Lymnaeoidea; Lymnaeidae; Lymnaea
NCBI_TaxID=6523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Johnsen A.H., Rehfeld J.F.;
"LymnaDFamides, a new family of neuropeptides from the pond snail,
Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eur. J. Biochem. 213:875-879(1993).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Related to the cholecystokinin (CCK) family
                                                        Score 30; DB 1; Length 11;
Pred. No. 3e+02;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 25, DB 1; Length 13; Pred. No. 2.6e+03; 3; Mismatches 2; Indels
 Phenylalanine amide.
7E4E0680E86B5AAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amidation; Direct protein sequencing; Neuropeptide. MOD RES 13 13 Phenylalanine amide. SEQUENCE 13 AA; 1519 MW; 9CA07BA3F5D5B455 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                    13 AA
                                                                                                                                                                                                                                                                                                                                                                               Lymnaea stagnalis (Great pond snail).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93238777; PubMed=8477756;
                                                                                                                                                                                                                                                                                                       01-JUL-1993 (Rel. 26, Created)
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Similarity 44.4%;
4; Conservative
 11 11
11 AA; 1459 MW;
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                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                   6 YDQYGHAAF 14
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2 YDRISNSAF 10
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                                                        Query Match
Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invertebrates?";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Ganglion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=NCU04977.1;
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P80178:
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SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- FUNCTION: Changes the frequency and amplitude of contractions of the cockroach hingut. Stimulates muscle contraction of hindgut.
-i- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
PIR; B60656; B60656.
InterPro; IPR001651; Gastrin.
PROSITE; PS00259; GASTRIN; 1.
Amidation; Direct protein sequencing; Hormone;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Isolation and structure of two gastrin/CCK-like neuropeptides from the American cockroach homologous to the leucosulfakinins."; Neuropeptides 14:145-149(1989).
                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90137190; PubMed=2615921; DOI=10.1016/0143-4179(89)90038-3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leucophaea maderae (Madeira cockroach).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
Blaberidae; Leucophaea.
                                                                                                                                                                                                       Periplaneta americana (American cockroach).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Orthopteroidea, Dictyoptera, Blattaria, Blattoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A01622; GMROL.
InterPro; IPR001651; Gastrin.
PROSITE; PS00259; GASTRIN; 1.
Amidation; Direct protein sequencing; Hormone; Sulfation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pyrrolidone carboxylic acid.
Phenylalanine amide.
9B4F539IE86BSAAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 31; DB 1; Pred. No. 1.8e+02;
                                                                                                       P67803; P09039;
01-NOV-1988 (Rel. 09, Created)
01-FBB-1994 (Rel. 28, Last sequence update)
15-CCT-2004 (Rel. 45, Last annotation update)
Leucosulfakinin-II (LSK-II)
Periplaneta americana (American cockroach).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
13-UUL-2004 (Rel. 44, Last annotation update)
Leucosulfakinin-I (LSK-I).
                                                                                             10 AA
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62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pyrrolidone carboxylic acid.
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                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                          FISSUE=Corpora cardiaca;
                                                                                                                                                                                                                                                                Blattidae, Periplaneta.
NCBI_TaxID=6978;
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Best Local Similarity
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DDYGHMRF 10
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SEQUENCE

LSK1 LEUMA P04428;

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10 LESKI LIA

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1; Indels

0; Mismatches

Score 24; DB 2; Length 16; Pred. No. 4.7e+03;

CEF73B5B28A4D952 CRC64;

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STRAIN=Berlin 1;
Yu H., Davis T.M.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF000217; A9436544.1;
GO; GO:0004022; F:alcohol dehydrogenase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
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16 16
16 AA; 1713 MW;
                                                                                                                                                                                                                                                                                                                                                                                          27.9%;
80.0%;
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Best Local Similarity 80.0°
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      [1]
SEQUENCE FROM N.A.
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082406
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082405
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Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S. Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A., DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R., Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R., Patvis D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M., Paulsen I., Sache M.S., Lander E.S., Nusbaum C., Birren B.; "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukāryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
NCBI_TaxID=60188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                               Nature 0:0-0(2003).
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBU whole genome shotgun (WGS) entry which is
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40.0%; Pred. No. 3.8e+03;
ive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yu H., Davis T.M., Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases. EMBL, APR00213; AAC36540.1; Go. GO:00044022; F:alcohol dehydrogenase activity; IEA. GO; GO:0016491; F:oxidoreductase activity; IEA.
                                                                                                                                                                                                                                                                                                      preliminary data.
; AABX01000422; EAA29651.1; -.
ENCE 13 AA; 1703 MW; 099245360492586B CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAX-2004 (TrEMBLrel. 26, Last annotation update)
Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).
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16 AA; 1682 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 AYDQYGHAAF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AIDYYGYCYY 11
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fragaria nubicola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 YGHAA 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=64941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=FRA520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=ADH;
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                                                                                                                                                                                                                                                                                                                                            EMBL;
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082402
002402
AC 08240
DT 01-NO
DT 08240
OC EURAR
OC EURAR
OC EURAR
OC STRAI
RA STRAI
RA STRAI
DR EMBL;
DR EMBL;
DR EMBL;
DR EMBL;
SC TRAI
SC TRAI
DR EMBL;
DR EMBL;
DR EMBL;
DR EMBL;
DR EMBL;
SC TRAI
SC TR
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082404
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DT 01-NC
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids 1; Rosales; Rosaceae; Rosoideae; Fragaria.
NCBL_TaxID=64940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                  Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; rosids, eurosids I; Rosales, Rosaceae, Rosoideae, Fragaria.
NCBI_TaxID=64939;
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Pred. No. 4.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=FRA 377;
Yu H., Davis T.M.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF000218; AAG36545.1; -.
GO; GO:0004022; F:alcohol dehydrogenase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CEF73B5B28A4D952 CRC64;
                                                                          01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).
16 AA
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                                                     Created)
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80.0%;
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                                               01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08,
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Gaps

.; 0

Score 24; DB 2; Length 16; Pred. No. 4.7e+03; 0; Mismatches 1; Indels

CEF73B5B28A4D817 CRC64;

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Yu H., Davis T.M.,
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                              EMBL; AF000216; AAC36543.1; -.
EMBL; AF000214; AAC36541.1; -.
GO; GO:0004022; F:alcohol dehydrogenase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
STRAIN-Yellow Wonder, and Baron Solemacher;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7, 2005, 09:57:54
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Similarity 80.0%;
4; Conservative
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Job time : 173 secs
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.

NCBI_TaxID=64942;
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                                                                                                                                                                                                                                                                                                                                                                                                                     27.9%; Score 24; DB 2; Length 16;
80.0%; Pred. No. 4.7e+03;
tive 0; Mismatches 1; Indels
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Pred. No. 4.7e+03;
0; Mismatches 1; Indels
                                                              STRAIN=FRA 341;
Yu H., Davis T.M.;
Submitted (APR-197) to the EMBL/GenBank/DDBJ databases.
EMBL; AF000220, AAC36547.1;
GO; GO:0004022; F:alcohol dehydrogenase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                   16 AA; 1713 MW; CEF73B5B28A4D952 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).
Name-ADH;
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nes 4; Conservative
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SEQUENCE 16 AA
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082781
1D 20228
AC 08278
DT 01-NO
DT 01-NO
DT 05-JU
DB Alcoh
DB Alcoh
CO Bukar
OC Bukar
OC Bukar
OC Suraga:
OC 
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082407
082407
082407
08240
08240
09240
001-NO
001-NO
001-NO
002 Bukar
003 Bragas
003 Bragas
004 Bukar
005 Bukar
006 Bukar
007 Bukar
007 Bukar
007 Bukar
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7, 2005, 09:07:16; Search time 159 Seconds (without alignments) 38.919 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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2105692 seqs, 386760381 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 1 OKRAAYDOYGHAAFEO 16 US-10-001-938-3 86 Perfect score: Scoring table: Sequence: Searched:

649094 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 16 88 Minimum Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* Geneseg 16Dec04:\* geneseqp2002s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Description	u988	Abr55126 E. coli d	Aaw25795 Peptide d	Aay79543 E. coli d	Aam99341 Vaccine r	Aau09842 E.coli dn	Aau98876 E. coli D	7 Hurt	Abr55132 E. coli D	Aam99344 Vaccine r		Aaw25796 Peptide d	Aae19458 Heat shoc	Abr55133 E. coli d	Aar95445 RA suscep	Pep	Abr55123 E. coli d	Aau03347 Fruit fly		_	Adel4680 Drosulfak	Ade14676 DmGPCR bi	Ade14679 DmGPCR bi	Ade14677 DmGPCR bi	Adl83524 Drosophil
a		ABR55126	AAW25795	AAY79543	AAM99341	AAU09842	AAU98876	AAE19457	ABR55132	AAM99344	AAR95446	AAW25796	AAE19458	ABR55133	AAR95445	AAW25798	ABR55123	AAU03347	AAU03346	AAU03351	ADE14680	ADE14676	ADE14679	ADE14677	ADL83524
99	'n	9	~	ო	4	S	ß	'n	9	4	~	~	Ŋ	9	~	0	9	4	4	4	7	7	7	7	7
% Query Match Length DB	16	16	15	15	15	15	15	15	15	16	. 15	15	15	15	14	15	15	σ	6	σ	6	δ	0	6	σ
% Query Match	100.0	100.0	94.2	94.2	94.2	94.2	94.2	94.2	94.2	94.2	83.7	83.7	83.7	83.7	75.0	62.8	62.8	39.5	39.5	39.5	39.5	39.5	39.5	39.8	39.5
Score	98	86	81	81	81	81	81	81	81	81	72	72	72	72	64.5	54	54	34	34	34	34	34	34	34	34
Result No.	п	7	٣	4	2	9	7	80	6	10	11	. 12	13	14	15	16	17	18	19	20	21	22	23	24	25

Ad181525 Drosophil Ad183603 Drosophil Ad183528 Drosophil Ad183527 Drosophil Ad102247 G-protein Adr01249 G-protein Adr01248 G-protein Adr01248 G-protein Adr01248 G-protein Adr01248 G-protein Adr01248 G-protein Adr01259 G-protein Adr01259 Drosophil Adr01251 Drosophil Adr01250 Drosophil Adr01250 Drosophil	Aaw25799 Synthetic
ADL83525 ADL83602 ADL83603 ADL83528 ADL83527 ADR03245 ADR03248 ADR03248 ADR03248 ADR03244 ADR03244 ADR03250 ADR03529 ADR03529 ADR03250 AAR10086 AAR10086	AAW25799
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### ALIGNMENTS

Immunogenic peptide; heat shock protein; HSP; DNAJ; immunomodulatory; cytostatic; antiinflammatory; antibacterial; antiarthritic; autoimmune disease; arthritis; articular juvenile idiopathic arthritis; inflectious disease; inflammatory bowel disease; cancer; mucosal tolerisation; DNA vaccination; anergy induction. E.Coli DNAJ 61 immunogenic peptide. AAU98852 standard; peptide; 16 AA. (first entry) 22-AUG-2002 AAU98852; RESULT 1 AAU98852 

Escherichia coli

WO200236611-A2. 10-MAY-2002. 31-OCT-2001; 2001WO-US045344.

01-NOV-2000; 2000US-0245181P.

(REGC ) UNIV CALIFORNIA. (MART/) MARTINI A.

Prakken BJ; Carson DA, Martini A, Albani S,

WPI; 2002-489999/52.

New immunomodulatory peptides from heat shock proteins, useful for treating immunological disorder in subjects such as humans, e.g. autoimmune disease (e.g. arthritis), infectious disease, inflammatory bowel disease or cancer.

Claim 4; Page 55; 84pp; English.

This invention relates to the use of a peptide, which is an immunogenic portion derived from a dnaJ heat shock protein (hsp) in modulating an immune response in a subject. The peptides of the invention may have immunomodulatory, cytostatic, antiinflammatory, antibacterial or antiarthritic properties and can stimulate expression of interleukins, tumour necrosis factor and transforming growth factor better. The immunogenic peptide is useful for modulating (i.e. augmenting) inducing or reducing/inhibiting) an immune response in a subject having an

Gaps

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Indels

Length 16;

Score 86; DB 6; I Pred. No. 4.7e-08;

Mismatches

100.08; Fr. 0; 100.08;

16; Conservative

Matches

Query Match Best Local Similarity

Sequence 16 AA;

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immunological disorder (e.g. autoimmune disease such as arthritis or articular juvenile idiopathic arthritis), an infectious disease, an inflammatory bowel disease or cancer. The immunogenic peptide of the invention is also useful for modulating immunoeffector cell responsiveness in a subject. The immunogenic peptide is particularly useful for treating the above-mentioned diseases in mammals, e.g. cat, dog, horse, farm animal (e.g. ovine, bovine or porcine) or human. In general, the peptide is useful in methods involving mucosal tolerisation, DNA vaccination, anergy induction or active immunisation. The present sequence represents an B. coli DNAJ immunogenic peptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modulating an immune response in a subject having an immune-related disorder, e.g. arthritis by administering an antigen-specific epitope and a cytokine or an agent that effects cytokine activity or expression.
                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coli dnaJ61 antigen-specific epitope peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABR55126 standard; peptide; 16 AA.
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Best Local Similarity 100.
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                                                                                                                                                                                                                           Sequence 16 AA;
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ABR55126
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arthritogenic peptide, autoimmune disease, systemic immune system; anti-dnaJpl antibody; passive immunisation; rheumatoid arthritis-susceptibility detection.

Escherichia coli.

WO9734002-A1.

18-SEP-1997.

97WO-US002957. 96US-00618464.

20-FEB-1997;

15-MAR-1996;

(REGC ) UNIV CALIFORNIA.

Peptide dnaJp1 which protects against arthritogenic peptides.

06-APR-1998 (first entry)

AAW25795;

AAW25795 standard; peptide; 15 AA.

RESULT 3

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protein; dnaJpl; adult rheumatoid arthritis; vaccine;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli. One peptide, dnaJpl (AAW25795) was found to a induce relatively strong immune response in seropositive adult theumatoid arthritis patients. This peptide was used in a vaccine for protecting against arthritogenic peptides. The vaccine contains a carrier, pure dnaJpl peptide or a recombinant gene expression vector encoding the dnaJpl peptide. The vaccines are used to prevent rheumatoid arthritis (or other autoimmune diseases). Vaccines can target the arthritogenic peptides before they are presented to the systemic immune system. Anti-danJpl antibodies can also be used for passive immunisation. Anti-danJpl antibodies can also be used for passive immunisation. Antibodies can be used to detect rheumatoid arthritis-susceptibility sequences on HIA or in populations of E. coli in the gastrointestinal tract
                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaccine for protecting against arthritogenic peptide(s) containing dnaJp1 - also determining pre-disposition to rheumatoid arthritis by detecting anti-arthritogenic peptide antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptides AAW25795-96 and AAW25798 are derived from the dnaJ protein from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 3.3e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Page 5, 44pp, English.
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100.0%; Pre
0; }
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                                                                                                                                                                                                                                                                                                                                                                       Carson DA, Albani S;
                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-470882/43.
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Best Local Similarity
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Matches
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modulating an immune response in a subject having an immune-related disorder. The present sequence is used in the exemplification of the

immunomodulator; antiallergic; endocrine; neuroprotectant; virucidal; bactericidal; antiparasitic; fungicidal; cytostatic; medicine; pharmaceutical; immune disorder; immune deficiency; autoimmune; hypersensitivity; allergy; graft rejection; infection; hormonal disorder; central nervous system disease; cancer; melanoma; anti-melanoma vaccine; human immunodeficiency virus.

Glutamic acid; glutamine; vaccine; major histocompatibility complex; MHC;

Vaccine related MHC ligand peptide SEQ ID NO:444.

07-DEC-2001 (first entry)

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This peptide is derived from Bscherichia coli heat shock protein dhadpl.

Novel artificial antigen presenting cells (APC) of the invention comprise antigens, such as the present peptide, that are presented by a major histocompatibility complex (MHC) component for contact with, and recognition by, a T cell receptor. The invention is directed to artificial APC and methods of making APC, which are used to isolate and expand T cell populations and to modulate T cell responses. The invention also provides novel methods for the identification and isolation of inposomes containing MHC; peptide complexes, accessory molecules, costimulatory molecules, adhesion molecules, and other molecules irrelevant to T cell binding or modulation that are used in the binding of corrections of antigen-specific T cells. Devices and methods are and identification and antigen-specific T cells. Devices and methods are continued for treating conditions that would benefit from modulation of T provided for treating conditions that would benefit from modulation of T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New artificial antigen presenting cells useful for isolating and expanding T cells, and modulating T cell responses for the treatment of e.g. autoimmune diseases, allergies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell response, e.g. autoimmune disorders (especially type I diabetes mellitus, multiple sclerosis, rheumatoid arthritis, dermatomiosytis, juvenile rheumatoid arthritis and uveitis), allergies, cancer, vifal
                                                                                                                                                        Antigen presenting cell; T-lymphocyte; T-cell; immunomodulator; autoimmune disease; allergy; cancer; infection; graft rejection; immunotherapy; therapy; major histocompability complex; MHC; dnaJpl;
                                                                                                                   B. coli dnaJp1 heat shock protein peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 42; 179pp; English.
AAY79543 standard; peptide; 15 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infections, and graft rejection
                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0105018P
                                                                                                                                                                                                                                                                                                                                                                                    19-OCT-1999; 99WO-US024666
                                                                             (first entry)
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                                                                                                                                                                                                                         heat shock protein.
                                                                                                                                                                                                                                                               Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ALBA/) ALBANI S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15 AA;
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                                                                             15-AUG-2000
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                                     AAY79543;
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Stabilized pharmaceutical containing N-terminal glutamic acid or glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt

Claim 9; Page 107; 149pp; French.

with strong acid.

Goetsch L;

Beck A,

Corvaia N,

WPI; 2001-611470/70. Klinguer-Hamour C,

(FABR ) FABRE MEDICAMENT SA PIERRE.

23-MAR-2000; 2000FR-00003711. 22-MAR-2001; 2001WO-FR000872.

WO200170772-A2 Homo sapiens

27-SEP-2001

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The present invention describes a pharmaceutical compound (1) that

contains an N-terminal glutamic acid (Glu) or glutamine (Gln) residue in

the form of an addition salt with a strong, physiologically acceptable

acid (II). Also described are: (a) a pharmaceutical composition

acid (II). Also described are: (b) a vaccine containing at least one (I)

where this is a major histocompatibility complex (MHC) ligand (Ia); (c) a

method for in vitro diagnosis of diseases associated with the presence of

(Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process

(Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process

(Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process

(Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process

(Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process

(Ia) in processor (c) the simmonodulator, endocrime, antiallergic,

in pharmaceutical compositions (for treating immune disorders, e.g.

treiction, infection, hormonal disorders and central nervous system

diseases), also, where (I) is a MHC ligand (Ia), in vaccines for

treatment or prevention of: (i) viral, bacterial, parasitic or fungal

infections; or (ii) of cancers. A particular application is in anti-

melanoma vaccines. (I) are also useful for in vitro diagnosis of diseases

ssociated with interactions between MHC and (I); e.g. melanoma and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               associated with interactions between MHC and (I), e.g. melanoma and human immunodeficiency virus infection. AAM98898 to AAM99592 represent peptides which can be used in pharmaceutical compounds from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Mismatches 0;
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100.0%; Fit
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tes 15; Conserv
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Score 81; DB 3; Length 15;

Pred. No. 3.3e-07; Mismatches 0;

94.2. 100.0%; Pre-

Local Similarity 100 tes 15; Conservative

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1 OKRAAYDQYGHAAFE 15

QKRAAYDQYGHAAFE

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94.28;

AAM99341 standard; peptide; 15 AA.

AAM99341 ID AAMS RESULT 5

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(ALBA/) ALBANI S.
                                                              Sequence 15 AA;
 26-FEB-2002
                  01-NOV-2001
                          Albani S;
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AAU98876;
RESULT 7
 4AU98876
     E.coli dnaJpl heat shock protein-derived peptide.
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(first entry)

Antigenic; antidiabetic; neuroprotective; antirheumatic; antiarthritic; dermatological; immunosuppressive; ophthalmological; antiallergic; cytostatic; virucide; antibacterial; artificial antigen presenting cell; liposome, major histocompatibility complex, MHC; T cell; allograft, cytokine production; T-helper 2 response; transplantation therapy; autoimmune disease, type I diabetes mallitus; multiple sclerosis; rheumatoid arthritis; dermatomyositis; juvenile rheumatoid arthritis; uveitis; dialergy; cancer; infection; dhaJpl heat shock protein.

Escherichia coli

WO200180833-A1

20-APR-2000; 2000WO-IT000161

20-APR-2000; 2000WO-IT000161

WPI; 2002-055316/07

New artificial antigen presenting cell, useful for modulating T cell response for treating allergies and cancers, comprises liposome, major histocompatibility complex, antigen and accessory molecule components.

Disclosure; Page 46; 195pp; English.

The invention relates to an artificial antigen presenting cell (I) comprising liposome, major histocompatibility complex (MHC), antigen and accessory molecule components. (I) is used in methods for the following: (I) identifying T cells specific for an antigen of interest; (3) modulating T cells specific for an antigen of interest; (3) modulating T cells specific for an antigen of interest; (3) modulating T cells response; (4) characterising the functional state of antigenspecific T cells; (5) treating a condition in a subject which would be certain antigen-specific T cells; (6) identifying antigen-specific T cells and/or decrease Thi response; (6) identifying antigen-specific T cells specific for epitopes on a graft donor's tissue likely to elicit graft versus host rejection response; and (7) treating a recipient mammal to reduce rejection of allografts in a transplantation therapy regime.

Method (5) is useful for treating autoimmune disease such as type I diabetes mellitus, multiple sclerosis, rheumatoid arthritis, demandroystis, juvenile rheumatoid arthritis or uveitis. Alternatively it is useful for treating allergy due to allergens such as dust, animal skin bypass products, vegetables, fruits, pollen or chemicals, cancer, viral infection, bacterial infection. Addition of the accessory molecules, as well as co-stimulatory molecules, and other protein in proper orientation in the liposomes allow for substantially improved binding association and manipulation of r cells which is very important in the identification and stimulation of antigen-specific T cells. The present sequence represents E.coli dnaupi heat shock protein-derived peptide used in the method of the invention

Gaps ö Length 15; Indels ö Score 81; DB 5; Le Pred. No. 3.3e-07; 0; Mismatches 0; 94.2., 100.0%; Pr. 0; Conservative Local Similarity les 15; Conserv Query Match Best Loc Matches

OKRAAYDOYGHAAFE 15

ÓKRAAYDOYGHAAFE 15

AAU98876 standard; peptide; 15 AA.

(first entry) 22-AUG-2002

E. coli DNAJ PI immunogenic peptide.

Immunogenic peptide; heat shock protein; HSP; DNAJ; immunomodulatory; cytostatic; antiinflammatory; antibacterial; antiarthritic; human; autoimmune disease; arthritis; articular juvenile idiopathic arthritis; infectious disease; inflammatory bowel disease; cancer; HDJ2; mucosal tolerisation; DNA vaccination; anergy induction.

Escherichia coli.

WO200236611-A2.

10-MAY-2002

31-OCT-2001; 2001WO-US045344.

01-NOV-2000; 2000US-0245181P.

(REGC ) UNIV CALIFORNIA. (MART/) MARTINI A.

Prakken BJ; Carson DA, Wartini A, Albani S,

WPI; 2002-489999/52.

New immunomodulatory peptides from heat shock proteins, useful for treating immunological disorder in subjects such as humans, e.g. autoimmune disease (e.g. arthritis), infectious disease, inflammatory bowel disease or cancer.

Example 8; Page 53; 84pp; English.

This invention relates to the use of a peptide, which is an immunogenic portion derived from a dnaJ heat shock protein (hsp) in modulating an immunome response in a subject. The peptides of the invention may have immunomedulatory, cytostatic, antiinflammatory, antibacterial or antiarthritic properties and can stimulate expression of interleukins, tumour necrosis factor and transforming growth factor beta. The immunogenic peptide is useful for modulating growth factor beta. The immunological disorder (e.g. autoimmune disease such as arthritis or immunological disorder (e.g. autoimmune disease such as arthritis or articular juvenile idiopathic arthritis), an infectious disease, an inflammatory bowel disease or cancer. The immunogenic peptide of the invention is also useful for modulating immunogenic peptide is particularly useful for treating the above-mentioned diseases in mammals, e.g. cat, dog, horse, farm animal (e.g. ovine, bovine or porcine) or human. In dog, horse, farm animal (e.g. ovine, bovine or porcine) or human. In general, the peptide is useful in methods involving mucosal tolerisation, DNA vaccination, anergy induction or active immunisation. The present sequence represents the R.coli DNAJ PI immunogenic peptide of the

Sequence 15 AA;

Gaps .; 0 94.2%; Score 81; DB 5; Length 15; 100.0%; Pred. No. 3.3e-07; ive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 15; Conservative

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Antigen-specific epitope, immune response, T cell, cytokine, antiarthritic; antidiabetic; neuroprotective; anti-inflammatory, cytostatic; antithyroid; anti-athmatic; immunosuppressive; antipsoriatic; anti-ulcer; antianaemic; cardiant; respiratory; antiallergic; dermatological; antipsoriatic.

25-SEP-2002; 2002WO-US030578. 25-SEP-2001; 2001US-0325499P. 11-DEC-2001; 2001US-0339284P.

03-APR-2003

Escherichia coli WO2003026579-A2. (REGC ) UNIV CALIFORNIA

Albani S,

B. coli DnaJpl antigen-specific epitope peptide.

03-JUL-2003 (first entry)

ABR55132;

ABR55132 standard; peptide; 15 AA.

RESULT

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Human; human leukocyte antigen; HLA; DR-binding peptide; therapy; stress protein; major histocompatibility complex; MHC; antiulcer; type I diabetes; scleroderma; heat shock protein; hsp; vitiligo; rheumatoid arthritis; lupus erythematcosus; myasthenia gravis; tumour; ulcerative colitis; infectious disease; haemostatic; nephrotropic; polymyositis; chronic active hepatitis; primary biliary cirrhopis; pernicious anaemia; autoimmune thyroiditis; Siogren's syndrome; cancer; grave's disease; autoimmune thyroiditis; Siogren's syndrome; cancer; inflammatory bowel disease; multiple sclerosis; hepatotropic; antimiacorbial; immunosuppressive; dermatological; antiinflammatory; antiinflammatory; antiinflammatory;
                                                                            Human heat shock protein (hsp) dnaJP1 peptide.
          AAE19457 standard; peptide; 15 AA
                                                                                                                                                                                                                                                                                                                                                             (UYCA-) UNIV CALIFORNIA SAN DIEGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 9; Page 45; 68pp; English.
                                                                                                                                                                                                                                                                                                      08-AUG-2001; 2001WO-US041656.
                                                                                                                                                                                                                                                                                                                             09-AUG-2000; 2000US-0224104P.
06-APR-2001; 2001US-00828574.
                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                    Prakken BJ;
                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-227137/28.
                                                                                                                                                                                                                                                           WO200212286-A2.
                                                                                                                                                                                                                                      Homo sapiens
                                                     31-MAY-2002
                                                                                                                                                                                                                                                                                 14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                    Albani S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention
                                AAE19457;
AAE19457
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peptide comprising a fragment of a stress protein that binds to one or more major histocompatibility complex (WHC) class II molecules. The invention also relates to hear shock protein (hap) peptides. The peptides of the invention and thr immunomodulating composition comprising these peptides are useful for modulating, treating or preventing an immunemediated disease in amammalian subject e.g. human, having or at risk of nediated disease in amammalian subject e.g. mulanoma, type I having a disease including autoimmune disease, multiple solarosis (WS), theumatoid arthritis, lupus erythematosus, myasthenia gravis, type I chaptoma, lackraemia, lung, liver, kidney, brain, bladder solat dumours, retinoblastoma, sarcoma and connective tissue cancers) and infectious inseases. The peptides of the invention are also useful for screening peptides or analogues that modulate pathogenic immune response. These peptides or analogues that modulate pathogenic immune response. These peptides are useful for treating autoimmune diseases or disorders including Sjogren's syndrome, polymyositis, chronic active hepatitis, mixed connective tissue disease, primary biliary cirrhosis, pernicious anaemia, autoimmune thyroiditis, vitiligo, idiopathic Addison's disease, gluten-sensitive enteropathy, Grave's disease, inflammatory bowel classase, pullous spenphiguid, discoid lupus and dense deposit disease. The present contemples are pemphiguid, discoid lupus, and dense deposit disease. The present
Novel human leukocyte antigen pan DR-binding peptide, useful for treating immune mediated diseases and conditions, has a fragment of stress protein that binds to major histocompatibility complex class II molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bullous pemphigoid, discoid lupus and dense deposit disease. The present
sequence is human hsp dnaJPl peptide used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                invention relates to human leukocyte antigen (HLA) pan DR-binding
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                                                                                                                                                                                                                                                                                                                          The invention relates to a novel method for modulating an immune response administering an antigen-related disorder. The method comprises: (a) administering an antigen-specific pelitope, where administration provides epitope-specific T cell immune modulation; and (b) administering a cytokine, an agent that effects cytokine activity or expression, or an anticycokine therapy. The method of the invention has antiarthritic, antidabetic, neuroprotective, anti-inflammatory, cytostatic, anti-asthmatic, immunosuppressive, antipsoriatic, anti-ulcer, antianaemic, cardiant, respiratory general, antiallergic, dermatological, and antipsoriatic activity. The method is useful for modulating an immune response in a subject having an immune-related disorder. The present sequence is used in the exemplification of the
                                                                                                                          disorder, e.g. arthritis by administering an antigen-specific epitope and a cytokine or an agent that effects cytokine activity or expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                  Modulating an immune response in a subject having an immune-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94.2%; Score 81; DB 6; Length 15; 100.0%; Pred. No. 3.3e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                    Disclosure; Page 9; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 OKRAAYDOYGHAAFE 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OKRAAYDQYGHAAFE 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100. Matches 15; Conservative
WPI; 2003-430097/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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RESULT 10 AAM99344

Length 15;

Score 81; DB 5; Le Pred. No. 3.3e-07;

94.2%; S 100.0%;

Query Match Best Local Similarity

Sequence 15 AA;

-∂

RA susceptibility sequence peptide #2.

(first entry)

01-JUL-1996

AAR95446;

AAR95446 standard; peptide; 15 AA.

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Glutamic acid; glutamine; vaccine; major histocompatibility complex; MHC; immunomodulator; antiallergic; endocrine; neuroprotectant; virucidal; bactericidal; antiparasitic; fungicidal; cytostatic; medicine; pharmaceutical; immune disorder; immune deficiency; autoimmune; yppersensitivity; allergy; graft rejection; infection; hormonal disorder; central nervous system disease; cancer; melanoma; anti-melanoma vaccine; human immunodeficiency virue.
                                                                                                                                                                                                                                                                                                                                                               Stabilized pharmaceutical containing N-terminal glutamic acid or glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt
                                                                  Vaccine related MHC ligand peptide SEQ ID NO:447.
                                                                                                                                                                                                                                                                                                                     Klinguer-Hamour C, Corvaia N, Beck A,
                                                                                                                                                                                                                                                                                              (FABR ) FABRE MEDICAMENT SA PIERRE,
 AAM99344 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Page 107; 149pp; French
                                                                                                                                                                                                                                                  22-MAR-2001; 2001WO-FR000872.
                                                                                                                                                                                                                                                                         23-MAR-2000; 2000FR-00003711.
                                            (first entry)
                                                                                                                                                                                                                                                                                                                                          WPI; 2001-611470/70.
                                                                                                                                                                                                                                                                                                                                                                          glutamine, useful with strong acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16 AA;
                                                                                                                                                                                                      WO200170772-A2
                                                                                                                                                                                  Homo sapiens
                                            07-DEC-2001
                                                                                                                                                                                                                             27-SEP-2001
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Goetsch L;

The present invention describes a pharmaceutical compound (1) that contains an N-terminal glutamic acid (Glu) or glutamine (Gln) residue in the form of an addition salt with a strong, physiologically acceptable acid (II). Also described are: (a) a pharmaceutical composition containing at least one (I); (b) a vaccine containing at least one (I) where this is a major histocompatibility complex (MiC) ligand (Ia); (c) a method for in vitro diagnosis of diseases associated with the presence of (Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process (Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process neuroprotectant, virucidal, bactericidal, antiparasitic, fungicidal and cytosfettic activities (I) are useful, in human or veterinary medicine, im pharmaceutical, compositions (for treating immune discretes e.g. immuno deficiency, autoimmune estates, hyporseneltivity, allergy, graft rejection, infection, hormonal disorders and central nervous system diseases), also, where (1) is a MHC ligand (1a), in vaccines for treatment or prevention of: (i) viral, bacterial, parasitic or fungal infections; or (ii) of cancers. A particular application is in antimenanom vaccines. (I) are also useful for in vitro diagnosis of diseases associated with interactions between MHC and (1), e.g. melanoma and human immunodeficiency virus infection. AAM98898 to AAM99592 represent peptides which can be used in pharmaceutical compounds from the present invention

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                                        Gaps
                                        ö
94.2%; Score 81; DB 4; Length 16; 100.0%; Pred. No. 3.6e-07; ive 0; Mismatches 0; Indels
                                                                   1 OKRAAYDQYGHAAFE 15
                Best Local Similarity 100.
Matches 15; Conservative
 Query Match
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OKRAAYDOYGHAAFE 15

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RESULT 11 AAR95446

2 KRAAYDQYGHAAFE 15

RESULT 12 AAW25796

AAR95445 and AAR95446 represent rheumatoid arthritis (RA) susceptibility sequence (see AAR95443 and AAR95444) containing peptides. This sequence corresponds to a region of dnaJ. These sequences are present on arthritogenic proteins and are targeted in this invention as antibody recognition sites. The anti-arthritogenic peptide antibodies that are developed can then be administered to a patient who has RA or who is peptides. The antibodies are produced and administered in milk. An alternative treatment method comprises the administration of a non-adsorbable antibodies are produced and administration of a non-adsorbable antibodie, together with a RA-begnign bacteria (selected from the genera Escherichia, Lactococcus, Klebsiella and Proteus), to the patient who has RA (or a predisposition to it). Candidates for either of these methods can be screened by detecting an in-vitro callular immune response to an arthritogenic peptide. The method of the invention allows (such as dnaJ). It also limits the exposure of the systemic immune system of humans to RA arthritogenic peptides present in the gastrointestinal ö Treatment of rheumatoid arthritis - by limiting exposure of immune system Rheumatoid arthritis, RA; dnaJ; E.coli; heat shock protein; antibody; arthritogenic peptide; RA-begnign bacteria; Escherichia; Lactococcus; Klebsiella; Proteus; therapy. .5 /note= "rheumatoid arthritis susceptibility sequence" Gaps ; Length 15; Indels Score 72; DB 2; Ler Pred. No. 1.3e-05; 1; Mismatches 0; Location/Qualifiers Example 3; Page 36; 52pp; English. 95WO-US004896 94US-00246988 /note= "K2E" to arthritogenic peptide(s). 83.7%; 92.9%; 13; Conservative Salvatore A; (REGC ) UNIV CALIFORNIA note= WPI; 1996-020344/02. Query Match Best Local Similarity Matches 13; Conserv Misc-difference Misc-difference Sequence 15 AA; 24-APR-1995; 20-MAY-1994; WO9531984-A1 30-NOV-1995 Carson DA, Synthetic Region

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Vaccine for protecting against arthritogenic peptide(s) containing dnaJpl - also determining pre-disposition to rheumatoid arthritis by detecting anti-arthritogenic peptide antibodies.
                                                                               dnaJ protein; dnaJpl; adult rheumatoid arthritis; vaccine;
arthritogenic peptide; autoimmune disease; systemic immune system;
                                                           Peptide dnaJpV which protects against arthritogenic peptides.
                                                                                                                                                                                 /label= Q1D
/note= "wild type Gln substituted with Asp"
                                                                                                                                                                                                                         /note= "wild type Lys substituted with Glu"
                                                                                                   anti-dnaJpl antibody; passive immunisation; rheumatoid arthritis-susceptibility detection.
                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 5; 44pp; English
standard; peptide; 15
                                                                                                                                                                                                                                                                                       97WO-US002957,
                                                                                                                                                                                                                                                                                                          96US-00618464.
                                                                                                                                                                                                                /label= K2E
                                       (first entry)
                                                                                                                                                                                                                                                                                                                             (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                 Carson DA, Albani S;
                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-470882/43.
                                                                                                                                Synthetic.
Escherichia coli.
                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15 AA;
                                        06-APR-1998
                                                                                                                                                                                                                                                                                      20-FEB-1997;
                                                                                                                                                                                                                                                                                                          15-MAR-1996;
                                                                                                                                                                                                                                              WO9734002-A1
                                                                                                                                                                                                                                                                   18-SEP-1997
 AAW25796
                     AAW25796;
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Peptides AAW25795-96 and AAW25798 are derived from the dnaJ protein from EBscherichia coli. One peptide, dnaJpl (AAW25795) was found to a induce relatively strong immune response in seropositive adult rheumatoid arthritis patients. This peptide was used in a vaccine for protecting against arthritogenic peptides. The vaccine contains a carrier, pure dnaJpl peptide or a recombinant gene expression vector encoding the dnaJpl peptide. The vaccines are used to prevent rheumatoid arthritis (or other autoimmune diseases). Vaccines can target the arthritogenic peptides before they are presented to the systemic immune system. AntidnaJpl antibodies can also be used for passive immunisation. AntidnaJpl antibodies can also be used for passive immunisation. Antibodies can be used to detect rheumatoid arthritis-susceptibility sequences on HLA or in populations of E. coli in the gastrointestinal tract
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Length 15; 0; Indels Score 72; DB 2; I Pred. No. 1.3e-05; Mismatches 1; 83.7%; 92.9%; 13; Conservative Query Match Best Local Similarity Matches

KRAAYDOYGHAAFE 15 ERAAYDOYGHAAFE 15

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AAE19458 RESULT 13 AAE19458 ID AAE1 XX AC AAE1

AAE19458 standard; peptide; 15 AA.

(first entry)

Heat shock protein (hsp) dnaJpV peptide.

Human leukocyte antigen; HLA; DR-binding peptide; therapy; stress protein; major histocompatibility complex; MHG; antiulcer; type I diabetes; scleroderma; heat shock protein; hsp; vitiligo; rheumatoid arthritis; lupus erythematosus; myasthenia gravis; tumour; ulcerative colitis; infectious disease; haemostatic; nephrotropic; polymyositis; chronic active hepatitis; primary biliary cirrhopis; pernicious anaemia; autoimmune thyroiditis; Slogren's syndrome; cancer; firstamentory bown disease; multiple sclerosis; hepatotropic; inflammatory bown disease; Goodpasture's syndrome; neuroprotective; antimicarobial; immunosuppressive; dermatological; antiinflammatory; antiinfertility; idiopathic Addison's disease; cytostatic.

Unidentified

WO200212286-A2

14-FEB-2002.

08-AUG-2001; 2001WO-US041656.

09-AUG-2000; 2000US-0224104P. 06-APR-2001; 2001US-00828574.

(UYCA-) UNIV CALIFORNIA SAN DIEGO.

Prakken BJ; Albani S,

WPI; 2002-227137/28.

Novel human leukocyte antigen pan DR-binding peptide, useful for treating immune mediated diseases and conditions, has a fragment of stress protein that binds to major histocompatibility complex class II molecules.

Example 3; Page 46; 68pp; English.

The invention relates to human leukocyte antigen (HLA) pan DR-binding peptide comprising a fragment of a stress protein that binds to one or more major histocompatibility complex (MHC) class II molecules. The peptide cinvention also relates to heat shock protein (hsp) peptides. The peptides of the invention and thr immunomodulating composition comprising these peptides are useful for modulating, treating or preventing an immunement of peptides are useful for modulating, treating or preventing an immunement of a disease in a mammalian subject e.g. human, having or at risk of thaving a disease including autoimmune disease, multiple sclerosis (MS), rheunatoid arthritis, lupus erychematosus, myaathenia gravis, type I diabetes, scleroderma, ulcerative colitis, cancer (e.g. melanoma, I usukaemia, lung, liver, kidney, brain, bladder solid tumours, retinoblastoma, sarcoma and connective tissue cancers) and infectious diseases. The peptides of the invention are also useful for screening peptides or analoguee that modulate pathogenic immune response. These peptides are useful for treating autoimmune diseases or disorders including Sjogran's syndrome, polymyositis, chronic active hepatitis, mixed connective tissue disease, primary biliary cirrhosis, pernicious anaemia, autoimmune thyroiditis, vitiligo, idiopathic Addison's disease, gluten-sensitive enteropathy, Grave's disease, inflammatory bowel disease, autoimmune neutropaenia, idiopathic thromobocytopaenia purpura, pemphigus vulgaris, autoimmune infertility, Goodpasture's syndrome, bullous pemphigoid, discoid lupus and dense deposit disease. The present sequence is hsp dnaJpV peptide used in the exemplification of the invention

Sequence 15 AA;

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Gaps

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Gaps ö Score 72; DB 5; Length 15; Pred. No. 1.3e-05; 1; Mismatches 0; Indels ch 83.7%; 1 Similarity 92.9%; 13; Conservative Local Similarity Query Match Best Loca Matches

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2 KRAAYDQYGHAAFE 15

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Rheumatoid arthritis; RA; dnaJ; E.coli; heat shock protein; antibody; arthritogenic peptide; RA-begnign bacteria; Escherichia; Lactococcus; Klebsiella; Proteus; therapy.

Escherichia coli.

Key Region

RA susceptibility sequence peptide #1.

01-JUL-1996 (first entry)

Location/Qualifiers 1. .5 /note= "rheumatoid arthritis susceptibility sequence"

95WO-US004896, 94US-00246988

24-APR-1995; 20-MAY-1994;

WO9531984-A1 30-NOV-1995 Salvatore A;

Carson DA,

WPI; 1996-020344/02.

(REGC ) UNIV CALIFORNIA

2 ERAAYDQYGHAAFE 15

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The invention relates to a novel method for modulating an immune response in a subject having an immune-related disorder. The method comprises: (a) administering an antigen-specific epitope, where administering provides epitope-specific T cell immune modulation; and (b) administering a cytokine, an agent that effects cytokine activity or expression, or an anticytokine therapy. The method of the invention has antiarthritic, antidiabetic, neuroprotective, anti-inflammatory, cytostatic, antithyroid, anti-asthmatic, immunesuppressive, antisposiatic, anti-ulcar, antianaemic, cardiant, respiratory general, antiallergic, modulating and antippositatic activity. The method is useful for modulating an immune response in a subject having an immune-related disorder. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modulating an immune response in a subject having an immune-related disorder, e.g. arthritis by administering an antigen-specific epitope and a cytokine or an agent that effects cytokine activity or expression.
                                                                                                                                                                                                                                                                                                                                                   Antigen-specific epitope, immune response, T cell, cytokine, antiarthritic, antidiabetic, neuroprotective, anti-inflammatory, cytostatic, antithyroid, anti-asthmatic, immunosuppressive, antipsoriatic, anti-ulcer, antianaemic, cardiant, respiratory,
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Pred. No. 1.3e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                        E. coli dnaJpV antigen-specific epitope peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiallergic; dermatological; antipsoriatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 9; 41pp; English
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                                                                      ABR55133 standard; peptide; 15 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-SEP-2002; 2002WO-US030578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83.7%;
92.9%;
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                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (REGC ) UNIV CALIFORNIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-430097/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003026579-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15 AA;
                                                                                                                                                                                                                  03-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Albani S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention
                                                                                                                                            ABR55133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR95445;
ABRES133
ABRES133
ABRES133
ABRES133
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ID AAR9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           원
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AAR95445 and AAR95446 represent rheumatoid arthritis (RA) susceptibility corresponds to a region of daal. These sequences are present on arthritogenic proteins and are targeted in this invention as antibody arthritogenic proteins and are targeted in this invention as antibody recognition sites. The anti-arthritogenic peptide antibodies that are developed can then be administered to a patient who has RA or who is predisposed to develop RA, to reduce the exposure to arthritogenic peptides. The antibodies are produced and administration of a nonalternative treatment method comprises the administration of a nonalternative treatment method comprises the administration of a nonalternative treatment are produced and administration of a nonalternative base RA (or a predisposition to it). Candidates for either of these methods can be screened by detecting an in-vitro cellular immune creapone to an arthritogenic peptide. The method of the invention allows for the reduction of sensitiaation to microbial arthritogenic peptides (such as dnay). It also limits the exposure of the systemic immune system of thumans to RA arthritogenic peptides present in the gastrointestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Treatment of rheumatoid arthritis - by limiting exposure of immune system to arthritogenic peptide(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 64.5; DB 2;
Pred. No. 0.00024;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Page 36; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 75.0%;
Best Local Similarity 93.3%;
Matches 14; Conservative
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Search completed: March 7, 2005, 09:54:55

Job time : 160 secs

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Gaps

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7, 2005, 09:58:03; Search time 130 Seconds (without alignments) . 40.498 Million cell updates/sec
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| Cgn2_6/ptodata/1/pubpaa/PCT_RFW PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/PCT_RFW PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/PCT_RFW PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US11AW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1391452 seqs, 329044822 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Sequence:
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                                                                                                                                                                                                                                                          Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	Sequence 3, Appli	Sequence 10, Appl	Sequence 10, Appl	Sequence 27, Appl	Sequence 4, Appli	Sequence 4, Appli	Sequence 444, App	Sequence 447, App		Sequence 5, Appli	Sequence 5, Appli	Sequence 6, Appli	
	ΩI	US-10-001-938-3	US-09-756-983-10	US-09-828-574-10	US-10-001-938-27	US-10-299-540-4	US-10-299-184-4	US-10-239-313A-444	US-10-239-313A-447	US-09-828-574-11	US-10-299-540-5	US-10-299-184-5	US-10-299-540-6	US-10-299-184-6
	DB	14	σ	σ	14						14	14	14	14
	Query Match Length DB	16	15	15	15	15	15	15	16	15	15	15	15	15
ф	Query Match	100.0	94.2	94.2	94.2	94.2	94.2	94.2	94.2	83.7	83.7	83.7	62.8	62.8
	Score	98	81	81	81	81	81	81	81	72	72	72	54	54
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RESULT 2 US-09-756-983-10

Sequence 154, App Sequence 155, App Sequence 157, App Sequence 158, App Sequence 159, App	154, 155, 159, 159,	- 200	Sequence 11, Appl Sequence 7, Appli Sequence 7, Appli Sequence 8, Appli Sequence 7, Appli Sequence 8, Appli Sequence 443, Appli	22225
23-1 23-1 23-1 23-1 23-1		16 US-10-736-048-157 16 US-10-736-048-159 14 US-10-161-959-6 14 US-10-283-423-160 14 US-10-213-821-160 15 US-10-736-048-160 17 US-10-845-407-6	US-09-756-983-1 US-10-161-959- US-10-299-540- US-10-299-184- US-10-299-184- US-10-239-313A	17 US-10-845-407-5 15 US-10-089-887-58 16 US-10-884-830-285 16 US-10-884-830-285 16 US-10-884-830-287
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#### ALIGNMENTS

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NESULY 1

US-10-01-938-3

Sequence 3, Application US/10001938

Sequence 3. Application US/10001938

Sequence 3. Application No. US2030031679A1

Sequence 3. Application No. US2030031679A1

Sequence 4. APLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA

APPLICANT: PARKEN, Dennis

APPLICANT: PARKEN, Dennis

APPLICANT: PARKEN, Dennis

TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES DERIVED FROM HEAT SHOCK PROTEINS AND US

TITLE OF INVENTION: IMMUNER: US/10/001,938

CURRENT FILING DATE: 2001-10-31

PRIOR APPLICATION NUMBER: US 60/245,181

PRIOR APPLICATION NUMBER: US 60/245,181

PRIOR APPLICATION NUMBER: US 60/245,181

SOFTWARE: PARENT OF US 05: 27

SOFTWARE: PRECED IN 05: 27

LENGTH: 16

TYPE: PRECED TO NOS: 27

COGRANISM: Escherichia coli

US-10-001-938-3

Query Match

Beet Local Similarity 100.0%; Pred. No. 9.2e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

MATCHES 16; CONSERVATOROHAAPEQ 16

Db 1 OKRAANDQYGHAAPEQ 16
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OF THE UNIVERSITY OF CALIFORNIA

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Patent No. US2002014675941

GENERAL INFORMATION:

APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA

APPLICANT: PRAKKEN, Berent J.

TITLE OF INVENTION:

FILE REFERENCE: UCSD1310-1

CURRENT APPLICATION NUMBER: US/09/828,574

CURRENT FILING DATE: 2001-04-06

PRIOR APPLICATION NUMBER: US 60/224,104

PRIOR FILING DATE: 2000-08-09

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin version 3.1

LENGTH: 15
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               GENERAL INCORPATION:
GENERAL INCORPATION:
GENERAL INCORPATION:
TITLE OF INVENTION: METHODS FOR ISOLATION, QUANTIFICATION,
TITLE OF INVENTION: CHARACTERIZATION AND MODULATION OF
TITLE OF INVENTION: ANTIGEN-SPECIFIC T CELLS;
FILE REPERENCE: 246/285-CTP
CURRENT APPLICATION NUMBER: US/09/756,983
CURRENT FILING DATE: 1099-10-09
PRIOR APPLICATION NUMBER: 00/421,506
PRIOR APPLICATION NUMBER: 09/421,506
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 24
NUMBER OF SEQ ID NOS: 24
COLD NOS: 24
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Pred. No. 6.1e-07;
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Pred. No. 6.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) OTHER INFORMATION: dnaJpl heat shock protein US-09-756-983-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 94.2%; Score 81; DB Best Local Similarity 100.0%; Pred. No. 6.1 Matches 15; Conservative 0; Mismatches
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US-10-001-938-27
is Sequence 27, Application US/10001938
is Publication No. US20030031679A1
igeneral INFORMATION:
Sequence 10, Application US/09756983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: dnaJP1 peptide
US-09-828-574-10
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Best Local Similarity 100.0%;
Matches 15; Conservative 0
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ORGANISM: Artificial sequence
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ORGANISM: E. coli
                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 10
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TITLE OF INVENTION: THEREOF
CURRENT APPLICATION NUMBER: US/10/001,938
CURRENT FILING DATE: 2001-10-31
PRIOR PELICHING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PAREOFIL OF SEQ ID NOS: 27
LENGTH: 15
TYPE: PRI
TYPE: TYPE: TREE
CORGANISM: Escherichia coli
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; Sequence 4, Application US/10299540
; Publication No. US20030143238A1
; GENERAL INFORMATION:
    APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: ALBANI, SALVACORE
; TITLE OF INVENTION: AGAINST ARTHRITOGENIC PEPTIDES INVOLVED IN THE PATHOGENESIS OF RI
; TITLE OF INVENTION: AGAINST ARTHRITOGENIC PEPTIDES INVOLVED IN THE PATHOGENESIS OF RI
; TITLE OF INVENTION: AGAINST ARTHRITOGENIC PEPTIDES INVOLVED IN THE PATHOGENESIS OF RI
; TITLE OF INVENTION: AGAINST ARTHRITOGENIC PEPTIDES INVOLVED IN THE PATHOGENESIS OF RI
; TITLE OF INVENTION: AGAINST ARTHRITOGENIC PEPTIDES INVOLVED IN THE PATHOGENESIS OF RI
; FILE OF INVENTION: AGAINST ASTRIBUTORS: US 90/616,247
; FILE REFERENCE: USD1370-7.14
; PRIOR FILING DATE: 2000-07-14
; PRIOR PELLING DATE: 1998-06-30
; PRIOR PELLING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 08/246,988
; PRIOR APPLICATION NUMBER: US 08/246,988
; PRIOR APPLICATION NUMBER: US 08/246,988
; PRIOR PILING DATE: 1994-05-20
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 4
; PRIOR PILING DATE: PATENTIAL 15
; ENG ID NO 4
; PRIOR PILING DATE: PATENTIAL 15
; ENG ID NO 4
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6.1e-07;
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. 6.1e-07;
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94.2%; Score 81; DB
Best Local Similarity 100.0%; Pred. No. 6.1
Matches 15; Conservative 0; Mismatches
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US-10-299-540-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-299-184-4 ; Sequence 4, Application US/10299184
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PRAKKEN, Berent
MARTINI, Alberto
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Best Local Similarity 100.
Matches 15; Conservative
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US-09-828-574-11

| Sequence 11, Application US/09828574
| Patent No. US20020146759A1
| Patent No. US20020146759A1
| GENERAL INPORMATION:
| APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
| APPLICANT: ALBANI, Salvatore
| APPLICANT: PRAKKEN, Berent J.
| TITLE OF INVENTION: STRESS PROTEINS AND PEPTIDES AND METHODS OF USE THEREOF
| PILE REFERENCE: USC01310-1
| CURRENT APPLICANTON NUMBER: US 60/224,104
| PRIOR PILING DATE: 2001-04-06
| PRIOR PILING DATE: 2000-08-09
| NUMBER OF SEQ ID NOS: 13
| SOFTWARE: Patentin version 3.1
| LENGTH: 15
                                                                                                                                                GREEAL INCOMATION:

GAPLICANT: CORVAIA, Nathalie

APPLICANT: CORVAIA, Nathalie

APPLICANT: CORVAIA, Nathalie

APPLICANT: BCK. Alain

APPLICANT: BCK. Alain

APPLICANT: GOETSCH, Liliane

TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS

TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID

TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID

FILE REFERENCE: 343 727 - US

CURRENT PELLING DATE: 2002-09-19

PRIOR PULLING DATE: 2000-03-23

PRIOR PELLING DATE: 2001-03-22

NUMBER OF SEQ ID NOS: 697

SEQ ID NO 447

LENGTH: 16

MANDER OF SEQ ID NOS: 697

LENGTH: 16

MANDER OF SEQ ID NOS: 697

LENGTH: 16
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Pred. No. 2.1e-05;
1; Mismatches 0; Indels
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Pred. No. 6.5e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                 ; Sequence 447, Application US/10239313A; Publication No. US20030175285A1; GENERAL INFORMATION:
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Best Local Similarity 100.0%; P

Matches 15; Conservative 0;
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92.9%;
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Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-10-239-313A-447
                                                            JS-10-239-313A-447
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Publication No. US20030147910A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: ALBANI, Salvatore
TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN INDUCING IMMUNE PROTEC
TITLE OF INVENTION: ARTHRITS
FILE REFERENCE: UCSD1370-6
CURRENT APPLICATION NUMBER: US 09/616,247
PRIOR APPLICATION NUMBER: US 09/616,247
PRIOR APPLICATION NUMBER: US 09/616,247
PRIOR PILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-03-15
PRIOR FILING DATE: 1998-03-15
PRIOR FILING DATE: 1994-05-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATCHIN VERSION 3.1
SEQ ID NOS: 10
SOFTWARE: PATCHIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: CORVAIA, Nathalie
APPLICANT: CORVAIA, Nathalie
APPLICANT: CORVAIA, Nathalie
APPLICANT: BCK., Alain
APPLICANT: BCK., Alain
APPLICANT: BCK., Alain
APPLICANT: GOETSCH, Liliane
TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
TITLE OF INVENTION: N-TERMINAL A GLUTAMINE IN THE FORM
TITLE OF INVENTION OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
FILE REFERENCE: 343 727 - US
CURRENT APPLICATION NUMBER: US/10/239, 313A
FRIOR PILING DATE: 2000-03-23
FRIOR PILING DATE: 2000-03-23
FRIOR FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 697
SOFTWARE: PATENTING UNE: 2.1
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Pred. No. 6.1e-07;
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; Sequence 444, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
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US-10-299-184-4
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Best Local Similarity 100.
Matches 15; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
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LENGTH: 15
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## FUDICARTION NO. US20030143238A1
### PEDICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
### PEDICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
### PEDICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
### PEDICANT: ALBANI, Salvatore
### TITLE OF INVENTION: AGAINST ARTHRITOGENIC PEPTIDES INVOLVED IN THE PATHOGENESIS OF RHITTLE OF INVENTION: ARTHRITIS
### PEDICATION: ARTHRITIS
### PEDICATION NUMBER: US/10/299,540
### CURRENT APPLICATION NUMBER: US 09/616,247
### PRIOR PILING DATE: 2000-07-14
### PRIOR PILING DATE: 1998-06-30
### PRIOR PILING DATE: 1998-06-30
### PRIOR PILING DATE: 1998-06-31
### PRIOR PILING DATE: 1994-05-20
### PRIOR PILING DATE: PRIOR PIL
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APPLICANT: CARSON, Dennis A.
APPLICANT: CARSON, Dennis A.
APPLICANT: ALBAIN, SALVACORE
TITLE OF INVENTION: AGAINST ARTHRITOGENIC PEPTIDES INVOLVED IN THE PATHOGENESIS OF RITILE OF INVENTION: AGAINST ARTHRITOGENIC PEPTIDES INVOLVED IN THE PATHOGENESIS OF RITILE OF INVENTION: AGAINST ARTHRITOGENIC PEPTIDES INVOLVED IN THE PATHOGENESIS OF RITILE OF INVENTION: AGAINST ARTHRITIS
FILLE OF INVENTION: AGAINST ARTHRITIS
FILLE OF INVENTION: AGAINST ARTHRITIS
FILLE OF INVENTION: AGAINST ASPLICATION NUMBER: US 09/616,247
PRIOR FILLING DATE: 1098-06-30
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1994-05-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NO 6
LENGTH: 15
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Pred. No. 0.024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Bacterial dnaJp2 peptide US-10-299-540-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/10299540 Publication No. US20030143238A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 62.8%; 8
Best Local Similarity 100.0%;
Matches 10; Conservative 0
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                                                       2 KRAAYDQYGHAAFE 15
                                                                                                     2 ERAAYDQYGHAAFE 15
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                                                               APPLICANT: THE RECENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: THE RECENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: CARSON, Dennis A.
APPLICANT: TALBANI, SALVACORE
TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODE USEFUL IN INDUCING IMMUNE PROTEC
TITLE OF INVENTION: AGAINST ARTHRITIS
TITLE OF INVENTION: AGAINST AGAINST AGAINST ARTHRITIS
TITLE OF INVENTION: AGAINST AGAINST AGAINST AGAINST APPLICATION NUMBER: US 09/616,247
PRIOR APPLICATION NUMBER: US 09/107,615
PRIOR FILING DATE: 1996-03-15
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APPLICANT: THE REGENTS
APPLICANT: CARSON, Dennis A.
APPLICANT: ALBANI, Salvatore
TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN INDUCING IMMUNE PROTE
TITLE OF INVENTION: ARTHHITIS
TITLE OF INVENTION: ARTHHITIS
TITLE OF INVENTION: ARTHHITIS
TITLE OF INVENTION: ARTHHITIS
FILE OF INVENTION: ARTHHITIS
TITLE OF INVENTION NUMBER: US 09/616,247
PRIOR PILING DATE: 2000-07-14
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1996-03-15
PRIOR FILING DATE: 1996-03-15
PRIOR FILING DATE: 1996-05-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATCHITIN VENSION 3.1
SEQ ID NO 5
LENGTH: 155
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Publication No. US20030143238A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 92.9%;
Matches 13; Conservative
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ORGANISM: Artificial sequence
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Best Local Similarity
Matches 13; Conserv
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Score 34; DB 14; Length >;
Pred. No. 1.3e+06;
3; Indels
PRIOR APPLICATION NUMBER: PriorAppNumber: 09/693,746
PRIOR FILING DATE: PriorFilingDate: 2000-10-20
PRIOR APPLICATION NUMBER: PriorAppNumber: 09/425,676
PRIOR FILING DATE: PriorFilingDate: 1999-10-22
NUMBER OF SEQ ID NOS: 187
SOFTWARE: PatentIn version 3.2
SEQ ID NO 155
LENGTH: 9
                                                                                                                                                                                                                                                                          , OTHER INFORMATION: No. US20030162223A1el Sequence
US-10-283-423-155
                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: March 7, 2005, 10:10:13
Job time: 130 secs
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                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 55.6%;
Matches 5; Conservative
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1 FDDYGHLRF 9
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APPLICANT: Smith, Valdin G.
APPLICANT: Smith, Valdin G.
APPLICANT: Kubiak, Teresa M.
APPLICANT: Larsen, Martha J.
TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method TITLE OF INVENTION: Related To The Same FILE REFERENCE: PHRM0002-102
Application Project
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APPLICANT: Smith, Valdin G.
APPLICANT: Kubiak, Teresa M.
APPLICANT: Larsen, Martha J.
APPLICANT: Larsen, Martha J.
TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method TITLE OF INVENTION: Related To The Same
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                                                                                                                                   62.8%; Score 54; DB 14; Length 15; 100.0%; Pred. No. 0.024; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PriorAppNumber: 09/693,746
PRIOR FILING DATE: PriorFilingDate: 2000-10-20
PRIOR APPLICATION NUMBER: PriorAppNumber: 09/425,676
PRIOR FILING DATE: PriorFilingDate: 1999-10-22
NUMBER OF SEQ ID NOS: 187
SOFTWARE: Patentin version 3.2
SEQ ID NO 154
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: No. US20030162223A1el Sequence
US-10-283-423-154
                                  FEATURE:
; OTHER INFORMATION: Bacterial dnaJp2 peptide
US-10-299-184-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/283,423 CURRENT FILING DATE: 2002-10-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 155, Application US/10283423; Publication No. US20030162223A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 154, Application US/10283423
Publication No. US20030162223A1
GENERAL INFORMATION:
              ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                Query Match 62.8
Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity
Matches 5; Conserv
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US-10-283-423-155
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US-10-283-423-154
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Scoring table:

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DENNIS A.
SALVATORE
VACCINE COMPOSITIONS AND METHODS USEFUL IN
IMMUNE PROTECTION AGAINST ARTHRITOC
                                                                                                                                                                                                                                                                                                                                                                                                                                               INVOLVED IN THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,464
                                                                                                                                                                                                                                                                                    US-08-618-464-4
; Sequence 4, Application US/08618464
; Patent No. 5773570
GENERAL INFORMATION:
APPLICANT: CARSON, DENNIS A.
APPLICANT: ALBANI, SALVATORE
TITLE OF INVENTION: INDUCING
TITLE OF INVENTION: INVOLVED IN
TITLE OF INVENTION: THE PATHOGENESIS OF RHEUM
NUMBER OF SEQUENCES: 8
CORRESPONDENCES: 8
CORRESPONDENCES: 8
CORRESPONDENCES: RICHARDSON P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CALIFORNIA
COUNTRY: US
                     FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGBAT INFORMATION:
NAME: HOWELLS, STACY L.
REGISTRATION NUMBER: 34,842
REPERENCE/DOCKET NUMBER: 07340/042001
TELECOMMUNICATION INFORMATION:
TELEFRONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.2%; Score 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunogenic dnaJ Peptide
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 92037
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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LOCATION:
US-08-618-464-4
Query Match
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Sequence 4, Appli
Sequence 5, Appli
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Sequence 154, App
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                                                                                         March 7, 2005, 09:52:27 ; Search time 41 Seconds
    (without alignments)
    29.131 Million cell updates/sec
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(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-160-615-4

US-09-160-986-4

US-09-161-986-5

US-09-107-615-5

US-09-107-615-5

US-09-107-615-6

US-09-693-746-154

US-09-693-746-157

US-09-693-746-159

US-09-693-746-159

US-09-693-746-159

US-09-693-746-159

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US-09-693-746-159

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US-09-693-746-160

US-09-107-615-8

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US-09-255-501-67
US-09-255-501-68
US-09-060-872A-67
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5-07-732-114A-5
5-08-170-114A-5
3-08-323-686-3
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                                                                                                                                                                                                                                                  513545 segs, 74649064 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                  - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QKRAAYDQYGHAAFE 15
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Best Local Similarity 100.
Matches 15; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 90012
                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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. VACCINE COMPOSITIONS AND METHODS USEFUL IN
. INDUCING IMMUNE PROTECTION AGAINST
ARTHRITOGENIC PEPTIDES INVOLVED IN
. THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
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                        0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/107,615
    Pred. No. 8.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                    E: FISH & RICHARDSON P.C.
4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Pred. No. 8.2
Matches 15; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING MAIL:
ATTORNEY/AGENT INFORMATION:
NAME: HOWELLS, STACY L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/042001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 aming acids
                        0; Mismatches
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APPLICATION NUMBER: US/08/618,464
FILING DATE:
                                                                                                                                                                                            Sequence 4. Application US/09107615
Fatent No. 6153200
GENERAL INFORMATION:
APPLICANT: CARSON, DENNIS A.
TITLE OF INVENTION: VACCINE COMPOS
TITLE OF INVENTION: UNDCING IMMUNITE OF INVENTION: TITLE OF INVENTION: THE PATHOGENES
CORRESPONDENCE ADDRESS:
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100.08;
                                                                                      1 OKRAAYDOYGHAAFE 15
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                        15; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) NAME/KEY: Peptide
; LOCATION: 1..15
US-09-107-615-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: La Jolla
STATE: CALIFORNIA
  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                US-09-107-615-4
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                        Matches
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RESULT 3 US-09-756-983-10 'Sequence 10, Application US/09756983 'Fatent No. 6787154

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Gaps
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APPLICANT: Albani, Salvatore
TITLE OF INVENTION: METHODS FOR ISOLATION, OUANTIFICATION,
TITLE OF INVENTION: CARACTERIZATION AND MODULATION OF
TITLE OF INVENTION: ANTIGEN-SPECIFIC T CELLS
TILLE REFERENCE: 246/285-CIP
CURRENT APPLICATION NUMBER: US/09/756,983
CURRENT PILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/105,018
PRIOR APPLICATION NUMBER: 60/105,018
PRIOR FILING DATE: 1999-10-19
PRIOR PILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: THE REGENTS OF THE UNIVERSITY
APPLICANT: OF CALIFORNIA
TITLE OF INVENTION: METHOD AND REAGENTS FOR THE TREATMENT
TITLE OF INVENTION: OF RHEUMATOID ARTHRITIS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 15;
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04896
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: BERLINER, ROBERT
REGISTRATION NUMBER: 20,121
REFRENCE/POCKET UNMBER: 5555-314
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.2%; Score 81; DB 4; L. 100.0%; Pred. No. 8.2e-08; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: ROBBINS, BERLINER & CARSON STREET: 201N. FIGUEROA STREET, 5TH FLOOR CITY: CITY: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: dnaJpl heat shock protein US-09-756-983-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
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TOPOLOGY: linear
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DENNIS A.
SALVATORE
VACCINE COMPOSITIONS AND METHODS USEFUL IN
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                                                                                                                                            INDUCING IMMUNE PROFECTION AGAINST
ARTHRITOGENIC PEPTIDES INVOLVED IN
THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY
APPLICANT: OF CALIFORNIA
ITILE OF INVENTION: METHOD AND REAGENTS FOR THE TREATMENT
ITILE OF INVENTION: OF RHEUMATOID ARTHRITIS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS: ADDRESSE: ROBEINS, BERLINER & CARSON
STREET: 201 N. FIGUEROA STREET, 5TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 15;
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                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 72; DB 3; I
Pred. No. 3.1e-06;
1; Mismatches 0;
                                                                                                                                                                             STREET: 4225 Executive Square, Suite 1400 CITY: La Jolla STATE: CALIFORNIA COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICALL...
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: HOWELLS, STACY L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/042001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/618,464
                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLONE: Immunogenic dnaJ Peptide
                                    Sequence 5, Application US/09107615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                   APPLICANT: ALBANI, SALVI, TITLE OF INVENTION: UAC, TITLE OF INVENTION: INDITITLE OF INVENTION: ARTITLE OF INVENTION: THE NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS: ADDRESSEE: FISH & RICH STREET: 4225 Executive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                      ZIP: 92037
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
US-09-107-615-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US95-04896-5
RESULT 6
US-09-107-615-5
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                                                                                                                                                                                                                                                                                                                                                       DENNIS A.
SALVATORE
SALVATORE
. VACCINE COMPOSITIONS AND METHODS USEFUL IN
IMMUNE PROTECTION AGAINST ARTHRITG
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                                                                                                                                                                                                                                                                                                                                                                                                                                 INVOLVED IN THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
                                                                                                           Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 15;
                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,464
                                                                                                           Score 81; DB 5; LA Pred. No. 8.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 72; DB 1; I
Pred. No. 3.1e-06;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISBE: FISH & RICHARDSON P.C.
1: 4225 Executive Square, Suite 1400
La Jolla
CALIFORNIA
                                                                                              94.2%; Score 100.0%; Pred. No. co. 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CIANGLES TO 424
ATTORNEY/AGENT INFORMATION:
NAME: HOWELLS, STACY L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/042001
TELEPHONE: 619/678-5070
TELEPHONE: 619/678-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunogenic dnaJ Peptide
 Immunogenic dnaJ Peptide
                                                                                                                                                                                                                                                                    RESULT 5
US-08-618-464-5
; Sequence 5, Application US/08618464
; Betent No. 5773570
; GENERAL INFORMATION:
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92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                     1 OKRAAYDOYGHAAFE 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KRAAYDQYGHAAFE 15
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ERAAYDQYGHAAFE 15
                                                                                          Ouery Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 15 amino acids
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Best Local Similarity 92.9
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: VA
TITLE OF INVENTION: IN
TITLE OF INVENTION: IN
TITLE OF INVENTION: IN
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & RI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Peptide LOCATION: 1..15
                                    Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: CARSON, APPLICANT: ALBANI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
US-08-618-464-5
                                   NAME/KEY:
; LOCATION:
PCT-US95-04896-4
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                      PEATURE
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Gaps
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, SALVATORE
. VACCINE COMPOSITIONS AND METHODS USEFUL IN
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ARTHRITOGENIC PEPTIDES INVOLVED IN
THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
                                                                                                                                                                                                                                                                                                                                                                               62.8%; Score 54; DB 1; Length 15; 100.0%; Pred. No. 0.0045; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRATI APPLICATION DATA:
APPLICATION NUMBER: US/09/107,615
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JENERAL IN.

APPLICANT: C.

APPLICANT: ALBAN.

TITLE OF INVENTION: N.

TITLE OF INVENTION: THE PATHOGENE.

TITLE OF INVENTION: THE PATHOGENE.

TITLE OF INVENTION: THE PATHOGENE.

CORRESPONDENCE ADDRESS:

ADDRESSEE: FISH & RICHARDSON P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Johla

TTEL JOHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PILING DATE:

CLASSIFTCATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/618,464
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: HOWELLS, STACY L.
REGISTRATION NUMBER: 34,842
REGISTRATION NUMBER: 34,842
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEPHONE: 619/678-5070
                  07340/042001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/09107615
Patent No. 6153200
GENERAL INFORMATION:
APPLICANT: CARSON, DENNIS A.
APPLICANT: ALBANI, SALVATORE
REGISTRATION NUMBER: 34,842
                REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
                                                 TELEPRAK: 619/678-5070
TELEPRAK: 619/678-5070
INPORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 15 amino acids TYPE: amino acidd STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 OKRAAYDOYG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 QKRAAYDQYG 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                     ; LOCATION:
US-08-618-464-6
                                                                                                                                                                                                                                                                              FEATURE:
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INVOLVED IN
THE PATHOGENESIS OF RHEUMATOID ARTHRITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 72; DB 5; Length 15;
Pred. No. 3.1e-06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARDERSEE: FISH & RICHARDSON P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CALIFORNIA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentln Naths:
APPLICATION NUMBER: US/08/618,464
                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04896
                                                                                                                                                                                                                                                                                                                     5555-314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: Immunogenic dnaJ Peptide
                                                                                                                                                                                             APPLICALLA
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: BERLINER, ROBERT
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555.
TELECOMMUNICATION INFORMATION:
TELEFAX: 219-977-1001
TELEFAX: 219-977-1001
TELEFAX: 219-977-1003
; INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
'TWATH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/08618464
Patent No. 5773570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , DENNIS A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.7%;
92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: HOWELLS, STACY L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 ERAAYDOYGHAAFE 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KRAAYDQYGHAAFE 15
                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: CARSON, DENN.
APPLICANT: ALBANI, SALVA
TITLE OF INVENTION: INDU
TITLE OF INVENTION: THE
NUMBER OF INVENTION: THE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Peptide / LOCATION: 1..15 PCT-US95-04896-5
LOS ANGELES
                CALIFORNIA
US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 13; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                       90012
                                       COUNTRY:
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US-08-618-464-6
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Sequence 157, Application US/09693746

Sequence 157, Application US/09693746

Sequence 157, Application US/09693746

GENERAL INFORMATION:

APPLICANT: Lowery, David E.

APPLICANT: Smith, Valdin G.

APPLICANT: Smith, Valdin G.

APPLICANT: Larsen, Martha J.

ITILE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method:

ITILE OF INVENTION: Related To The Same

FILE REFERENCE: 6297.1cp

CURRENT FILING DATE: 2000-10-20

FRIOR APPLICATION NUMBER: 09/425,676

FRIOR APPLICATION NUMBER: 09/425,676

FRIOR APPLICATION NUMBER: 09/425,676

SRICH RING DATE: 1999-10-22

NUMBER OF SEQ ID NOS: 168

SOFTWARE: Patentin version 3.1

IERNOR O. 157
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APPLICANT: Smith, Valdin G.
APPLICANT: Smith, Valdin G.
APPLICANT: Smith, Valdin G.
APPLICANT: Smith, Valdin G.
APPLICANT: Largen, Martha J.
TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method TITLE OF INVENTION: Related To The Same FILE REFERENCE: 6297.1cp
CURRENT APPLICATION NUMBER: US/09/693,746
CURRENT FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/425,676
PRIOR APPLICATION NUMBER: 09/425,676
PRIOR APPLICATION NUMBER: 1999-10-22
NUMBER OF SEQ ID NOS: 168
SOFTWARE: Patentin version 3.1
SEQ ID NO 158
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                                                                                          Score 34; DB 4; Length 9;
Pred. No. 4.1e+05;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: No. 6835546el Sequence US-09-693-746-158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: No. 6835546el Sequence
US-09-693-746-157
; FEATURE:
; OTHER INFORMATION: No. 6835546el Sequence
US-09-693-746-155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 158, Application US/09693746 Patent No. 6835546 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                        h 39.5%;
Similarity 55.6%;
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 55.6
Matches 5; Conservative
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1 FDDYGHLRF 9
                                                                                                                                                                                                                     : | | | | |
1 FDDYGHLRF 9
                                                                                                                   Best Local Similarity
Matches 5; Conserv
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US-09-693-746-157
                                                                                               Query Match
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US-09-693-746-154

i Sequence 154, Application US/09693746

j Patent No. 6835546

i GENERAL INFORMATION:

APPLICANT: Lowery, David E.

APPLICANT: Smith, Valdin G.

APPLICANT: Kubiak, Teresa M.

APPLICANT: Kubiak, Teresa M.

APPLICANT: Aresa Martha J.

TITLE OF INVENTION: Related To The Same

FILE REFERENCE: 6297.1cp

CURRENT APPLICATION NUMBER: US/09/693,746

CURRENT APPLICATION NUMBER: 09/425,676

PRIOR APPLICATION NUMBER: 09/425,676

PRIOR APPLICATION NUMBER: 09/425,676

PRIOR APPLICATION NUMBER: 09/425,676

NUMBER OF SEQ ID NOS: 168

SOUTHARE: Patentin version 3.1

SEQ ID NO 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 155, Application US/09693746

Sequence 155, Application US/09693746

Sequence 155, Application US/09693746

GENERAL INFORMATION:
APPLICANT: Lowery, David B.
APPLICANT: Smith, Valdin G.
APPLICANT: Larsen, Marcha J.
TITLE OF INVENTION: Related To The Same
FILE REFERENCE: 6297.1cp
CURRENT APPLICATION NUMBER: US/09/693,746

CURRENT FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/425,676

PRIOR APPLICATION NUMBER: 09/425,676

PRIOR PILING DATE: 1999-110-22

NUMBER OF SEQ ID NOS: 168

SOFTWARE: Patentin version 3.1

SEQ ID NO 155
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                                                                                                                                                                 Length 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39.5%; Score 34; DB 4; 1
llarity 55.6%; Pred. No. 4.1e+05;
Conservative 1; Mismatches 3;
                                                                                                                                                                 Score 54; DB 3; 1
Pred. No. 0.0045;
                                                                                                                                                                 Ouery Match 62.8%; Score 54; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , OTHER INFORMATION: No. 6835546el Sequence US-09-693-746-154
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ORGANISM: Artificial Sequence
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Matches 5; Conserv
    IMMEDIATE SOURCE:
                                                                    ; NAME/KEY:
; LOCATION:
US-09-107-615-6
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Sequence 159, Application US/09693746

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APPLICANT: Smith, Valdin G.
APPLICANT: Smith, Valdin G.
APPLICANT: Smith, Valdin G.
APPLICANT: Kublak, Teresa M.
APPLICANT: Larsen, Martha J.
TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Method TITLE OF INVENTION: Related To The Same TITLE OF INVENTION: Related To The Same CURRENT APPLICATION NUMBER: US/09/693,746
CURRENT APPLICATION NUMBER: 09/425,676
PRIOR PRING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 168
SOFTWARE: Patentin Version 3.1
SEQ ID NO 160
LENGTH: 14
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                                                                            3; Indels
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Pred. No. 14;
Query Match 39.5%; Score 34; DB 4; Length 9; Best Local Similarity 55.6%; Pred. No. 4.1e+05; Matches 5; Conservative 1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: No. 6835546el Sequence
US-09-693-746-159
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US-09-693-746-160
Sequence 160, Application US/09693746
Patent No. 6835546
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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1 FDDYGHMRF 9
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Best Local Similarity
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US-09-693-746-159
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Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps
Qy 6 YDQYGHARF 14
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Db 6 FDDYGHRRF 14
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Search completed: March 7, 2005, 10:07:26 Job time: 41 secs